

SEQUENCE LISTING

- <110> Genentech, Inc.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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- <140> 09/665,350
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- <150> PCT/US00/04414
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- <150> US 60/143,048
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- <150> US 60/145,698
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- <150> US 60/146,222
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- <150> PCT/US99/20944
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Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
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Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
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 <213> Homo sapiens

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100120-071001

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 <223> Description of Artificial Sequence: Synthetic
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<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<213> Homo sapiens

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<213> Homo sapiens

0902903-071004

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35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
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Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
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Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
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Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
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<211> 24

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<210> 21

<211> 44

<212> DNA

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100120-2052000

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35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
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Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
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Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
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Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
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Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
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Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 25

<211> 24
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 <223> a, t, c or g

<400> 26
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41

<210> 27
 <211> 2479
 <212> DNA
 <213> Homo sapiens

<400> 27
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 cttttttcct gaagtcttgg cttatcattt ccttggggct ctactcacag gtgtccaaac 360
 tcctggcctg ccctagtgtg tgccgctcgc acaggaactt tgtctactgt aatgagcgaa 420
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```

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

```

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
  1                      5                      10                      15

```

```

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
          20                      25                      30

```

```

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
          35                      40                      45

```

```

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
          50                      55                      60

```

```

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
          65                      70                      75                      80

```

```

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
          85                      90                      95

```

```

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
          100                      105                      110

```

```

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
          115                      120                      125

```

F00120-200200

Leu	Ala	Gln	Leu	Leu	Lys	Leu	Glu	Glu	Leu	His	Leu	Asp	Asp	Asn	Ser
130						135						140			
Ile	Ser	Thr	Val	Gly	Val	Glu	Asp	Gly	Ala	Phe	Arg	Glu	Ala	Ile	Ser
145			150						155			160			
Leu	Lys	Leu	Leu	Phe	Leu	Ser	Lys	Asn	His	Leu	Ser	Ser	Val	Pro	Val
			165						170			175			
Gly	Leu	Pro	Val	Asp	Leu	Gln	Glu	Leu	Arg	Val	Asp	Glu	Asn	Arg	Ile
			180			185						190			
Ala	Val	Ile	Ser	Asp	Met	Ala	Phe	Gln	Asn	Leu	Thr	Ser	Leu	Glu	Arg
195						200						205			
Leu	Ile	Val	Asp	Gly	Asn	Leu	Leu	Thr	Asn	Lys	Gly	Ile	Ala	Glu	Gly
210			215						220						
Thr	Phe	Ser	His	Leu	Thr	Lys	Leu	Lys	Glu	Phe	Ser	Ile	Val	Arg	Asn
225			230						235			240			
Ser	Leu	Ser	His	Pro	Pro	Pro	Asp	Leu	Pro	Gly	Thr	His	Leu	Ile	Arg
			245						250			255			
Leu	Tyr	Leu	Gln	Asp	Asn	Gln	Ile	Asn	His	Ile	Pro	Leu	Thr	Ala	Phe
			260			265						270			
Ser	Asn	Leu	Arg	Lys	Leu	Glu	Arg	Leu	Asp	Ile	Ser	Asn	Asn	Gln	Leu
275						280						285			
Arg	Met	Leu	Thr	Gln	Gly	Val	Phe	Asp	Asn	Leu	Ser	Asn	Leu	Lys	Gln
290			295						300						
Leu	Thr	Ala	Arg	Asn	Asn	Pro	Trp	Phe	Cys	Asp	Cys	Ser	Ile	Lys	Trp
305			310						315			320			
Val	Thr	Glu	Trp	Leu	Lys	Tyr	Ile	Pro	Ser	Ser	Leu	Asn	Val	Arg	Gly
			325			330						335			
Phe	Met	Cys	Gln	Gly	Pro	Glu	Gln	Val	Arg	Gly	Met	Ala	Val	Arg	Glu
			340			345						350			
Leu	Asn	Met	Asn	Leu	Leu	Ser	Cys	Pro	Thr	Thr	Thr	Pro	Gly	Leu	Pro
355						360						365			
Leu	Phe	Thr	Pro	Ala	Pro	Ser	Thr	Ala	Ser	Pro	Thr	Thr	Gln	Pro	Pro
370			375						380						
Thr	Leu	Ser	Ile	Pro	Asn	Pro	Ser	Arg	Ser	Tyr	Thr	Pro	Pro	Thr	Pro
385			390						395			400			
Thr	Thr	Ser	Lys	Leu	Pro	Thr	Ile	Pro	Asp	Trp	Asp	Gly	Arg	Glu	Arg

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttgagca agcggcggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60
cgctccccc gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

100740-04004


```
<210> 34
<211> 915
<212> PRT
<213> Homo sapiens
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Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
1 5 10 15

Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
145 150 155 160

Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser
				165					170					175	

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225		230		235		240
Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
	245	250	255			
Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260	265	270			
Asp Gln Thr Thr	Cys Arg Ile Gln Asp	Leu Cys Ala Met	Glu Asp His			
	275	280	285			
Asn Cys Glu Gln	Leu Cys Val Asn Val	Pro Gly Ser Phe	Val Cys Gln			
	290	295	300			
Cys Tyr Ser Gly	Tyr Ala Leu Ala	Glu Asp Gly Lys	Arg Cys Val Ala			
305	310	315	320			
Val Asp Tyr Cys	Ala Ser Glu Asn His	Gly Cys Glu His	Glu Cys Val			
	325	330	335			
Asn Ala Asp Gly	Ser Tyr Leu Cys	Gln Cys His Glu	Gly Phe Ala Leu			
	340	345	350			
Asn Pro Asp Glu	Lys Thr Cys Thr	Arg Ile Asn Tyr	Cys Ala Leu Asn			
	355	360	365			
Lys Pro Gly Cys	Glu His Glu Cys	Val Asn Met Glu	Glu Ser Tyr Tyr			
	370	375	380			
Cys Arg Cys His	Arg Gly Tyr Thr	Leu Asp Pro Asn	Gly Lys Thr Cys			
385	390	395	400			
Ser Arg Val Asp	His Cys Ala Gln	Gln Asp His Gly	Cys Glu Gln Leu			
	405	410	415			
Cys Leu Asn Thr	Glu Asp Ser Phe	Val Cys Gln Cys	Ser Glu Gly Phe			
	420	425	430			
Leu Ile Asn Glu	Asp Leu Lys Thr	Cys Ser Arg Val	Asp Tyr Cys Leu			
	435	440	445			
Leu Ser Asp His	Gly Cys Glu Tyr	Ser Cys Val Asn	Met Asp Arg Ser			
	450	455	460			
Phe Ala Cys Gln	Cys Pro Glu Gly	His Val Leu Arg	Ser Asp Gly Lys			
465	470	475	480			
Thr Cys Ala Lys	Leu Asp Ser Cys	Ala Leu Gly Asp	His Gly Cys Glu			
	485	490	495			
His Ser Cys Val	Ser Ser Glu Asp	Ser Phe Val Cys	Gln Cys Phe Glu			
	500	505	510			

100120-000000

Gly	Tyr	Ile	Leu	Arg	Glu	Asp	Gly	Lys	Thr	Cys	Arg	Arg	Lys	Asp	Val
		515				520						525			
Cys	Gln	Ala	Ile	Asp	His	Gly	Cys	Glu	His	Ile	Cys	Val	Asn	Ser	Asp
		530				535						540			
Asp	Ser	Tyr	Thr	Cys	Glu	Cys	Leu	Glu	Gly	Phe	Arg	Leu	Ala	Glu	Asp
		545				550						555		560	
Gly	Lys	Arg	Cys	Arg	Arg	Lys	Asp	Val	Cys	Lys	Ser	Thr	His	His	Gly
				565						570				575	
Cys	Glu	His	Ile	Cys	Val	Asn	Asn	Gly	Asn	Ser	Tyr	Ile	Cys	Lys	Cys
		580						585						590	
Ser	Glu	Gly	Phe	Val	Leu	Ala	Glu	Asp	Gly	Arg	Arg	Cys	Lys	Lys	Cys
		595				600						605			
Thr	Glu	Gly	Pro	Ile	Asp	Leu	Val	Phe	Val	Ile	Asp	Gly	Ser	Lys	Ser
		610				615						620			
Leu	Gly	Glu	Glu	Asn	Phe	Glu	Val	Val	Lys	Gln	Phe	Val	Thr	Gly	Ile
		625				630				635				640	
Ile	Asp	Ser	Leu	Thr	Ile	Ser	Pro	Lys	Ala	Ala	Arg	Val	Gly	Leu	Leu
				645						650				655	
Gln	Tyr	Ser	Thr	Gln	Val	His	Thr	Glu	Phe	Thr	Leu	Arg	Asn	Phe	Asn
		660						665						670	
Ser	Ala	Lys	Asp	Met	Lys	Lys	Ala	Val	Ala	His	Met	Lys	Tyr	Met	Gly
		675				680						685			
Lys	Gly	Ser	Met	Thr	Gly	Leu	Ala	Leu	Lys	His	Met	Phe	Glu	Arg	Ser
		690				695						700			
Phe	Thr	Gln	Gly	Glu	Gly	Ala	Arg	Pro	Leu	Ser	Thr	Arg	Val	Pro	Arg
		705				710				715				720	
Ala	Ala	Ile	Val	Phe	Thr	Asp	Gly	Arg	Ala	Gln	Asp	Asp	Val	Ser	Glu
				725				730						735	
Trp	Ala	Ser	Lys	Ala	Lys	Ala	Asn	Gly	Ile	Thr	Met	Tyr	Ala	Val	Gly
		740						745						750	
Val	Gly	Lys	Ala	Ile	Glu	Glu	Glu	Leu	Gln	Glu	Ile	Ala	Ser	Glu	Pro
		755				760						765			
Thr	Asn	Lys	His	Leu	Phe	Tyr	Ala	Glu	Asp	Phe	Ser	Thr	Met	Asp	Glu
		770				775						780			
Ile	Ser	Glu	Lys	Leu	Lys	Lys	Gly	Ile	Cys	Glu	Ala	Leu	Glu	Asp	Ser
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```
<210> 37
<211> 45
<212> DNA
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

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1813

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<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

100720-000000

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380

Gln Ala Gly Ser Leu Val
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

100120-071001

24

<400> 48						
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gtgaaatacg	caatggaatt	gaagcctgct	attgcaacat	gggattttca	ggaaatggtg	180
tcacaatttg	tgaagatgat	aatgaatgtg	gaaatttaac	tcagtcctgt	ggcgaaaatg	240
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atctttccacc	aaacagataa	attacatata	tagaaatttt	agctgaatca	tcttcattac	540
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aattttgtaaa	aaccgtgaat	aattttgttc	aaagggatac	atttgtagtt	tgggacaagt	660
tatctgtgaa	tcataggaga	acacatctta	caaaactcat	gcacactgtt	gaacaagcta	720
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gcaatgttgc	agttgcattt	ttatatatta	agagtattgg	tcctttgctt	tcatcatctg	960
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<210> 49
<211> 690
<212> PRT
<213> Homo sapiens
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<400> 49																
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Ser	Gly	Asn	Gly	Val	Thr	Ile	Cys	Glu	Asp	Asp	Asn	Glu	Cys	Gly	Asn	
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Leu	Thr	Gln	Ser	Cys	Gly	Glu	Asn	Ala	Asn	Cys	Thr	Asn	Thr	Glu	Gly	
65					70					75					80	
Ser	Tyr	Tyr	Cys	Met	Cys	Val	Pro	Gly	Phe	Arg	Ser	Ser	Ser	Asn	Gln	
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			100					105					110			
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Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr	
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Leu Arg
690

<211> 589

<213> Homo sapiens

<221> modified base

<222> (61)

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 55

ggatctcctg agtcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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100720-000000

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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
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His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
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Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
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<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 62
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<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
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<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
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 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30

100720-00020000

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Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	Leu	Glu	Trp	Lys		
50		55						60									
Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	Gln	Gln	Thr	Leu	Gln		
65		70						75							80		
Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	Asp	Phe	Asn	Ile	Arg	Ile		
85				90						95							
Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	Lys	Tyr	Arg	Cys	Glu	Val	Ser		
100			105						110								
Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	Leu	Glu	Glu	Asp	Thr	Val	Thr	Leu		
115		120						125									
Glu	Val	Leu	Val	Ala	Pro	Ala	Val	Pro	Ser	Cys	Glu	Val	Pro	Ser	Ser		
130		135						140									
Ala	Leu	Ser	Gly	Thr	Val	Val	Glu	Leu	Arg	Cys	Gln	Asp	Lys	Glu	Gly		
145		150						155						160			
Asn	Pro	Ala	Pro	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Arg	Leu	Leu		
165				170						175							
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180			185						190								
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195		200						205									
Thr	Gly	Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Ser	Val	Gly	Tyr	Arg	Arg		
210		215						220									
Cys	Pro	Gly	Lys	Arg	Met	Gln	Val	Asp	Asp	Leu	Asn	Ile	Ser	Gly	Ile		
225		230						235						240			
Ile	Ala	Ala	Val	Val	Val	Val	Ala	Leu	Val	Ile	Ser	Val	Cys	Gly	Leu		
245				250						255							
Gly	Val	Cys	Tyr	Ala	Gln	Arg	Lys	Gly	Tyr	Phe	Ser	Lys	Glu	Thr	Ser		
260			265						270								
Phe	Gln	Lys	Ser	Asn	Ser	Ser	Ser	Lys	Ala	Thr	Thr	Met	Ser	Glu	Asn		
275		280						285									
Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Lys	Ala	Ala	Ala		
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Gly	Gly	Ser	Arg	Gly	Gln	Glu	Phe										

305

310

<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 65

atcgttgtga agttagtgcc cc

22

<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 66

acctgcgata tccaacagaa ttg

23

<210> 67

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

48

<210> 68

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 68

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F00120-606666

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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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20 25 30

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35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
50 55 60

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Ile	Ala	Lys	Ile	Glu 85	Tyr	Ser	Thr	Asp	Phe 90	Pro	Val	Asn	Leu	Thr 95	Gly
Leu	Asp	Leu	Ser 100	Gln	Asn	Asn	Leu	Ser 105	Ser	Val	Thr	Asn	Ile 110	Asn	Val
Lys	Lys	Met 115	Pro	Gln	Leu	Leu	Ser 120	Val	Tyr	Leu	Glu	Glu 125	Asn	Lys	Leu
Thr	Glu 130	Leu	Pro	Glu	Lys	Cys 135	Leu	Ser	Glu	Leu	Ser 140	Asn	Leu	Gln	Glu
Leu 145	Tyr	Ile	Asn	His 150	Asn	Leu	Leu	Ser	Thr	Ile 155	Ser	Pro	Gly	Ala	Phe 160
Ile	Gly	Leu	His 165	Asn	Leu	Leu	Arg	Leu 170	His	Leu	Asn	Ser	Asn	Arg 175	Leu
Gln	Met	Ile 180	Asn	Ser	Lys	Trp	Phe	Asp 185	Ala	Leu	Pro	Asn	Leu 190	Glu	Ile
Leu	Met 195	Ile	Gly	Glu	Asn	Pro	Ile 200	Ile	Arg	Ile	Lys	Asp 205	Met	Asn	Phe
Lys 210	Pro	Leu	Ile	Asn	Leu	Arg 215	Ser	Leu	Val	Ile	Ala 220	Gly	Ile	Asn	Leu
Thr 225	Glu	Ile	Pro	Asp 230	Asn	Ala	Leu	Val	Gly	Leu 235	Glu	Asn	Leu	Glu	Ser 240
Ile	Ser	Phe 245	Tyr	Asp	Asn	Arg	Leu	Ile 250	Lys	Val	Pro	His	Val 255	Ala	Leu
Gln	Lys	Val 260	Val	Asn	Leu	Lys	Phe	Leu 265	Asp	Leu	Asn	Lys	Asn 270	Pro	Ile
Asn	Arg 275	Ile	Arg	Arg	Gly	Asp	Phe 280	Ser	Asn	Met	Leu	His 285	Leu	Lys	Glu
Leu 290	Gly	Ile	Asn	Asn	Met	Pro 295	Glu	Leu	Ile	Ser	Ile 300	Asp	Ser	Leu	Ala
Val 305	Asp	Asn	Leu	Pro	Asp 310	Leu	Arg	Lys	Ile	Glu 315	Ala	Thr	Asn	Asn	Pro 320
Arg	Leu	Ser 325	Tyr	Ile	His	Pro	Asn	Ala 330	Phe	Phe	Arg	Leu	Pro 335	Lys	Leu
Glu	Ser	Leu	Met	Leu	Asn	Ser	Asn	Ala	Leu	Ser	Ala	Leu	Tyr	His	Gly

[illegible]

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Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70
<211> 1305
<212> DNA
<213> Homo sapiens

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<210> 71
<211> 259
<212> PRT
<213> Homo sapiens

<400> 71

GGGCGGCAAGGT

<210> 72
<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

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5

10

15

F00720-202600

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Ser	Val	Leu	Ser	Gly	Ser	Ala	Thr	Gly	Cys	Pro	Pro	Arg	Cys	Glu	Cys	
		35						40						45		
Ser	Ala	Gln	Asp	Arg	Ala	Val	Leu	Cys	His	Arg	Lys	Cys	Phe	Val	Ala	
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Val	Pro	Glu	Gly	Ile	Pro	Thr	Glu	Thr	Arg	Leu	Leu	Asp	Leu	Gly	Lys	
65					70						75			80		
Asn	Arg	Ile	Lys	Thr	Leu	Asn	Gln	Asp	Glu	Phe	Ala	Ser	Phe	Pro	His	
					85						90			95		
Leu	Glu	Glu	Leu	Glu	Leu	Asn	Glu	Asn	Ile	Val	Ser	Ala	Val	Glu	Pro	
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Gly	Ala	Phe	Asn	Asn	Leu	Phe	Asn	Leu	Arg	Thr	Leu	Gly	Leu	Arg	Ser	
		115						120						125		
Asn	Arg	Leu	Lys	Leu	Ile	Pro	Leu	Gly	Val	Phe	Thr	Gly	Leu	Ser	Asn	
		130						135						140		
Leu	Thr	Lys	Gln	Asp	Ile	Ser	Glu	Asn	Lys	Ile	Val	Ile	Leu	Leu	Asp	
145					150						155			160		
Tyr	Met	Phe	Gln	Asp	Leu	Tyr	Asn	Leu	Lys	Ser	Leu	Glu	Val	Gly	Asp	
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Leu	Glu	Gln	Leu	Thr	Leu	Glu	Lys	Cys	Asn	Leu	Thr	Ser	Ile	Pro	Thr	
		195						200						205		
Glu	Ala	Leu	Ser	His	Leu	His	Gly	Leu	Ile	Val	Leu	Arg	Leu	Arg	His	
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Pro	Asn	Cys	Leu	Tyr	Gly	Leu	Asn	Leu	Thr	Ser	Leu	Ser	Ile	Thr	His	
		260						265						270		
Cys	Asn	Leu	Thr	Ala	Val	Pro	Tyr	Leu	Ala	Val	Arg	His	Leu	Val	Tyr	
		275						280						285		
Leu	Arg	Phe	Leu	Asn	Leu	Ser	Tyr	Asn	Pro	Ile	Ser	Thr	Ile	Glu	Gly	
		290						295						300		

Ser	Met	Leu	His	Glu	Leu	Leu	Arg	Leu	Gln	Glu	Ile	Gln	Leu	Val	Gly
305					310					315					320
Gly	Gln	Leu	Ala	Val	Val	Glu	Pro	Tyr	Ala	Phe	Arg	Gly	Leu	Asn	Tyr
				325					330					335	
Leu	Arg	Val	Leu	Asn	Val	Ser	Gly	Asn	Gln	Leu	Thr	Thr	Leu	Glu	Glu
			340					345					350		
Ser	Val	Phe	His	Ser	Val	Gly	Asn	Leu	Glu	Thr	Leu	Ile	Leu	Asp	Ser
		355					360					365			
Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Val	Phe	Arg	Arg	Arg
	370					375					380				
Trp	Arg	Leu	Asn	Phe	Asn	Arg	Gln	Gln	Pro	Thr	Cys	Ala	Thr	Pro	Glu
385					390					395					400
Phe	Val	Gln	Gly	Lys	Glu	Phe	Lys	Asp	Phe	Pro	Asp	Val	Leu	Leu	Pro
				405					410					415	
Asn	Tyr	Phe	Thr	Cys	Arg	Arg	Ala	Arg	Ile	Arg	Asp	Arg	Lys	Ala	Gln
			420					425					430		
Gln	Val	Phe	Val	Asp	Glu	Gly	His	Thr	Val	Gln	Phe	Val	Cys	Arg	Ala
		435					440					445			
Asp	Gly	Asp	Pro	Pro	Pro	Ala	Ile	Leu	Trp	Leu	Ser	Pro	Arg	Lys	His
	450					455					460				
Leu	Val	Ser	Ala	Lys	Ser	Asn	Gly	Arg	Leu	Thr	Val	Phe	Pro	Asp	Gly
465					470					475					480
Thr	Leu	Glu	Val	Arg	Tyr	Ala	Gln	Val	Gln	Asp	Asn	Gly	Thr	Tyr	Leu
				485					490					495	
Cys	Ile	Ala	Ala	Asn	Ala	Gly	Gly	Asn	Asp	Ser	Met	Pro	Ala	His	Leu
			500					505					510		
His	Val	Arg	Ser	Tyr	Ser	Pro	Asp	Trp	Pro	His	Gln	Pro	Asn	Lys	Thr
		515					520					525			
Phe	Ala	Phe	Ile	Ser	Asn	Gln	Pro	Gly	Glu	Gly	Glu	Ala	Asn	Ser	Thr
	530					535					540				
Arg	Ala	Thr	Val	Pro	Phe	Pro	Phe	Asp	Ile	Lys	Thr	Leu	Ile	Ile	Ala
545					550					555					560
Thr	Thr	Met	Gly	Phe	Ile	Ser	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Leu
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<210> 74
<211> 22
<212> DNA
<213> Artificial Sequence
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<400> 74
tcacctggag cctttattgg cc 22
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<400> 75
ataccagcta taaccaggct gcg                                     23
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<210> 76
<211> 52
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<400> 76
caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg 50
gg                                                    52
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<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 77
 ccatgtgtct cctcctacaa ag 22

<210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 78
 gggaatagat gtgatctgat tgg 23

<210> 79
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 79
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<210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 80
 agcaaccgcc tgaagctcat cc 22

<210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 81
 aaggcgcggt gaaagatgta gacg 24

<210> 82

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 82
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<400> 83
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 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

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Pro	Trp	Thr 35	Ser	Asp	Glu	Thr	Val 40	Val	Ala	Gly	Gly	Thr 45	Val	Val	Leu
Lys	Cys 50	Gln	Val	Lys	Asp	His 55	Glu	Asp	Ser	Ser	Leu 60	Gln	Trp	Ser	Asn
Pro 65	Ala	Gln	Gln	Thr	Leu 70	Tyr	Phe	Gly	Glu	Lys 75	Arg	Ala	Leu	Arg	Asp 80
Asn	Arg	Ile	Gln	Leu 85	Val	Thr	Ser	Thr	Pro 90	His	Glu	Leu	Ser	Ile 95	Ser
Ile	Ser	Asn 100	Val	Ala	Leu	Ala	Asp	Glu 105	Gly	Glu	Tyr	Thr 110	Cys	Ser	Ile
Phe	Thr 115	Met	Pro	Val	Arg	Thr	Ala 120	Lys	Ser	Leu	Val 125	Thr	Val	Leu	Gly
Ile 130	Pro	Gln	Lys	Pro	Ile	Ile 135	Thr	Gly	Tyr	Lys 140	Ser	Ser	Leu	Arg	Glu
Lys 145	Asp	Thr	Ala	Thr	Leu 150	Asn	Cys	Gln	Ser	Ser 155	Gly	Ser	Lys	Pro	Ala 160
Ala	Arg	Leu	Thr	Trp 165	Arg	Lys	Gly	Asp	Gln 170	Glu	Leu	His	Gly 175	Glu	Pro
Thr	Arg	Ile 180	Gln	Glu	Asp	Pro	Asn	Gly 185	Lys	Thr	Phe 190	Thr	Val	Ser	Ser
Ser	Val 195	Thr	Phe	Gln	Val	Thr	Arg 200	Glu	Asp	Asp	Gly 205	Ala	Ser	Ile	Val
Cys 210	Ser	Val	Asn	His	Glu	Ser 215	Leu	Lys	Gly	Ala 220	Asp	Arg	Ser	Thr	Ser
Gln 225	Arg	Ile	Glu	Val	Leu 230	Tyr	Thr	Pro	Thr	Ala 235	Met	Ile	Arg	Pro	Asp 240
Pro	Pro	His	Pro	Arg 245	Glu	Gly	Gln	Lys	Leu 250	Leu	Leu	His	Cys 255	Glu	Gly
Arg	Gly	Asn 260	Pro	Val	Pro	Gln	Gln	Tyr 265	Leu	Trp	Glu	Lys 270	Glu	Gly	Ser
Val	Pro 275	Pro	Leu	Lys	Met	Thr	Gln 280	Glu	Ser	Ala	Leu 285	Ile	Phe	Pro	Phe

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87
 cctagcacag tgacgaggga cttggc 26

<210> 88
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 88
 aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 89
 gccctggcag acgaggggga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
 <211> 2755
 <212> DNA
 <213> Homo sapiens

<400> 90
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1                      5                      10          15

```

```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
      20                      25          30

```

```

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
      35                      40          45

```

```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
      50                      55          60

```

```

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
      65                      70          75          80

```

```

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
      85                      90          95

```

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380

	660		665		670
Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp					
	675		680		685
Cys Gly Ser His Ser Leu Ser Asp					
	690		695		
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<210>	92				
<211>	22				
<212>	DNA				
<213>	Artificial Sequence				
<220>					
<223>	Description of Artificial Sequence: Synthetic				
	oligonucleotide probe				
<400>	92				
g tt g gat ctg gg ca a ca ata ac					22
<210>	93				
<211>	24				
<212>	DNA				
<213>	Artificial Sequence				
<220>					
<223>	Description of Artificial Sequence: Synthetic				
	oligonucleotide probe				
<400>	93				
att g tt gt gc ag g ct gag tt ta ag					24
<210>	94				
<211>	45				
<212>	DNA				
<213>	Artificial Sequence				
<220>					
<223>	Description of Artificial Sequence: Synthetic				
	oligonucleotide probe				
<400>	94				
g gt g g ct ata cat g gat agc a att ac ct gg ac ac g ct gt c cc g g g					45
<210>	95				
<211>	2226				
<212>	DNA				
<213>	Homo sapiens				
<400>	95				
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g ct g c ac cg g c ct g g c ag c g t c c g c a ca cat t t c ct gt c g c g g c c t aa g g g aa act gt	120				
t g g c c g ct gg g c c c g c g g g g g g att c t t gg c ag t t g g g g g g t c c g t c g g g ag c g ag g g g c g	180				

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<210> 96
<211> 490
<212> PRT
<213> Homo sapiens
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Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
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Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
50 55 60

Arg 65	Ala	Gly	Ala	Glu	Leu	Arg	Ala	Val	Leu	Ala	Leu	Leu	Arg	Ala	Gly 80
Pro	Gly	Pro	Gly	Gly	Gly	Ser	Lys	Asp	Leu	Leu	Phe	Trp	Val	Ala	Leu
				85					90					95	
Glu	Arg	Arg	Arg	Ser	His	Cys	Thr	Leu	Glu	Asn	Glu	Pro	Leu	Arg	Gly
			100					105					110		
Phe	Ser	Trp	Leu	Ser	Ser	Asp	Pro	Gly	Gly	Leu	Glu	Ser	Asp	Thr	Leu
		115					120					125			
Gln	Trp	Val	Glu	Glu	Pro	Gln	Arg	Ser	Cys	Thr	Ala	Arg	Arg	Cys	Ala
	130					135					140				
Val 145	Leu	Gln	Ala	Thr	Gly	Gly	Val	Glu	Pro	Ala	Gly	Trp	Lys	Glu	Met 160
					150					155					
Arg	Cys	His	Leu	Arg	Ala	Asn	Gly	Tyr	Leu	Cys	Lys	Tyr	Gln	Phe	Glu
			165						170					175	
Val	Leu	Cys	Pro	Ala	Pro	Arg	Pro	Gly	Ala	Ala	Ser	Asn	Leu	Ser	Tyr
			180					185					190		
Arg	Ala	Pro	Phe	Gln	Leu	His	Ser	Ala	Ala	Leu	Asp	Phe	Ser	Pro	Pro
		195					200					205			
Gly	Thr	Glu	Val	Ser	Ala	Leu	Cys	Arg	Gly	Gln	Leu	Pro	Ile	Ser	Val
	210					215					220				
Thr 225	Cys	Ile	Ala	Asp	Glu	Ile	Gly	Ala	Arg	Trp	Asp	Lys	Leu	Ser	Gly 240
					230					235					
Asp	Val	Leu	Cys	Pro	Cys	Pro	Gly	Arg	Tyr	Leu	Arg	Ala	Gly	Lys	Cys
				245					250					255	
Ala	Glu	Leu	Pro	Asn	Cys	Leu	Asp	Asp	Leu	Gly	Gly	Phe	Ala	Cys	Glu
			260					265					270		
Cys	Ala	Thr	Gly	Phe	Glu	Leu	Gly	Lys	Asp	Gly	Arg	Ser	Cys	Val	Thr
		275					280					285			
Ser	Gly	Glu	Gly	Gln	Pro	Thr	Leu	Gly	Gly	Thr	Gly	Val	Pro	Thr	Arg
	290					295					300				
Arg 305	Pro	Pro	Ala	Thr	Ala	Thr	Ser	Pro	Val	Pro	Gln	Arg	Thr	Trp	Pro 320
					310					315					
Ile	Arg	Val	Asp	Glu	Lys	Leu	Gly	Glu	Thr	Pro	Leu	Val	Pro	Glu	Gln
				325					330					335	
Asp	Asn	Ser	Val	Thr	Ser	Ile	Pro	Glu	Ile	Pro	Arg	Trp	Gly	Ser	Gln

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<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence
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<400> 97
tqgaaggaga tqcgatgcca cctg 24

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 98	
tgaccagtgg ggaaggacag	20

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<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens
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<400> 103

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cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
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gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

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Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20              25              30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35              40              45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50              55              60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
 275 280 285
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

100120-00000000

	340		345		350										
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro
	355						360					365			
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu
	370					375					380				
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys
385					390					395					400
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys	
			405						410					415	

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

F00T20-E00E0000

<213> Homo sapiens

<400> 108

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```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
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Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
  20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
  35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
  50              55              60

```

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
 65 70 75 80
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
 85 90 95
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
 100 105 110
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
 115 120 125
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
 130 135 140
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
 145 150 155 160
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
 165 170 175
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
 180 185 190
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
 195 200 205
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 210 215 220
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 225 230 235 240
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 245 250 255
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 260 265 270
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 275 280 285
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 290 295 300
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
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 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350

F00120-00000000

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365
 Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380
 Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400
 Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415
 Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

100120-00000000

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113
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 cagcaccatg cagccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcaccccca cccacgtgag 240
 ggcccagtag gtggccctgc tgcagcgcag ccacggggag cgctcccgcg gaaagaggtt 300
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360
 gctggtgttc ggcattggagc agcggctgcc gcccaacagc gagctggtgc aggcctgtgt 420
 gcggctcttc caggagccgg tccccaggc cgcgctgcac aggcacgggc ggctgtcccc 480
 gcgcagcgcc cggggccggg tgaccgtcga gtggtgcgc gtccgcgacg acggctccaa 540
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 cgacgtgacc gaggcctga acttctggca gcagctgagc cggccccggc agccgctgct 660
 gctacagggtg tcggtgcaga gggagcatct gggcccgcgt gcgtccggcg cccacaagct 720
 ggtcgcgttt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780
 caccctggac cttggggact atggagctca gggcgactgt gacctgaag caccaatgac 840
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960
 gcagcccccg gaggccttg ccttcaagtg gccgtttctg gggcctcgac agtgcctgcg 1020
 ctcgagact gactcgtgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080
 ccagggtggtc agcctgccc acatgagggt gcagaagtgc agctgtgcct cggatggtgc 1140
 gctcgtgcca aggaggctcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200
 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260
 ggacaaatgc tctgtgctct ctagttagcc ctgaatttgc ttctctgac aagttacctc 1320
 acctaatatt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380
 ttctctatcc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440
 acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500
 aaagtccctc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 1 5 10 15
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
 20 25 30
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

100120-00000000

Glu 50	Glu	Leu	Val	Ile	Pro	Thr 55	His	Val	Arg	Ala	Gln 60	Tyr	Val	Ala	Leu
Leu 65	Gln	Arg	Ser	His	Gly 70	Asp	Arg	Ser	Arg	Gly 75	Lys	Arg	Phe	Ser	Gln 80
Ser	Phe	Arg	Glu	Val 85	Ala	Gly	Arg	Phe	Leu	Ala	Leu	Glu	Ala	Ser 95	Thr
His	Leu	Leu	Val 100	Phe	Gly	Met	Glu	Gln 105	Arg	Leu	Pro	Pro	Asn 110	Ser	Glu
Leu	Val	Gln 115	Ala	Val	Leu	Arg	Leu	Phe	Gln	Glu	Pro	Val 125	Pro	Lys	Ala
Ala 130	Leu	His	Arg	His	Gly	Arg 135	Leu	Ser	Pro	Arg	Ser 140	Ala	Arg	Ala	Arg
Val 145	Thr	Val	Glu	Trp	Leu 150	Arg	Val	Arg	Asp	Asp 155	Gly	Ser	Asn	Arg	Thr 160
Ser	Leu	Ile	Asp	Ser 165	Arg	Leu	Val	Ser	Val	His	Glu	Ser	Gly	Trp 175	Lys
Ala	Phe	Asp	Val 180	Thr	Glu	Ala	Val	Asn 185	Phe	Trp	Gln	Gln	Leu 190	Ser	Arg
Pro	Arg	Gln 195	Pro	Leu	Leu	Leu	Gln 200	Val	Ser	Val	Gln	Arg 205	Glu	His	Leu
Gly 210	Pro	Leu	Ala	Ser	Gly	Ala 215	His	Lys	Leu	Val	Arg 220	Phe	Ala	Ser	Gln
Gly 225	Ala	Pro	Ala	Gly	Leu 230	Gly	Glu	Pro	Gln	Leu 235	Glu	Leu	His	Thr	Leu 240
Asp	Leu	Gly	Asp	Tyr 245	Gly	Ala	Gln	Gly	Asp 250	Cys	Asp	Pro	Glu	Ala 255	Pro
Met	Thr	Glu	Gly 260	Thr	Arg	Cys	Cys	Arg	Gln 265	Glu	Met	Tyr	Ile 270	Asp	Leu
Gln	Gly	Met 275	Lys	Trp	Ala	Glu	Asn 280	Trp	Val	Leu	Glu	Pro 285	Pro	Gly	Phe
Leu 290	Ala	Tyr	Glu	Cys	Val	Gly 295	Thr	Cys	Arg	Gln	Pro 300	Pro	Glu	Ala	Leu
Ala 305	Phe	Lys	Trp	Pro	Phe 310	Leu	Gly	Pro	Arg	Gln 315	Cys	Ile	Ala	Ser	Glu 320
Thr	Asp	Ser	Leu	Pro 325	Met	Ile	Val	Ser	Ile 330	Lys	Glu	Gly	Gly	Arg 335	Thr

```
<400> 118
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ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcttgagaat 180
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```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactggt atcaccttca agtcctgtgac acgggaagac 360
actgggacat acacttgatg ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc acctctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccccgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaagtctg tgcgcatgga agctgtggag cggaatgtgg gggtcacgtg ggcagccgtc 780
cttgtaaccc tgattctcct gggaatcttg gtttttggca tctggtttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtccccgaa gtgaaggaga attcaaacag acctcgatc tcttgggtgtg agcctggctg 960
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accgtgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaat acaaagttag ccaggcatgg tgggtcatgc ctgtagtccc 1800
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```

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

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Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1              5              10              15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
      20              25              30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
      35              40              45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
      50              55              60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
      65              70              75              80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
      85              90              95

```

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
 245 250 255
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

<210> 121

<211> 50

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

```
<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence
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```
<400> 122
acacctggtt caaagatggg                20
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```
<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 123
taggaagagt tgctgaaggc acgg 24

```
<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 124
ttgccttact caggtgctac 20

```
<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125

actcagcagt ggtaggaaag

20

<210> 126

<211> 1210

<212> DNA

<213> Homo sapiens

<400> 126

cagcgcgtgg cggcgccgc tgtggggaca gcatgagcgg cggttggatg gcgcagggtg 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctccgactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagtcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggaact gcagcgatgg cagcgatgag gaggagtgc 300
ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccc 360
gcaccggcgt cagtgaactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgtgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gacctggag agtgtccct 660
ctgtcgggaa tgccacatcc tctctgccc gagaccagtc tggagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagt caagcctggc caccgccacc ctctccttt 780
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ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960
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agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc 1210

<210> 127

<211> 282

<212> PRT

<213> Homo sapiens

<400> 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
65 70 75 80

F00T40-E00E0000

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
 225 230 235 240
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 129
 ttggttccac agccgagctc gtcg 24

<210> 130
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 130
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131
 <211> 1843
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1837)
 <223> a, t, c or g

<400> 131
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 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccga 180
 gcaatggaga tggatttcta gacgagcagc agcagcagca gcaacctcag tccccccaga 240
 gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcgccct gcacagctca 300
 cgggcgggtt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
 ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
 gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactc 540
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600
 atgaaggatt caagatccgg taccgacgac tacacaatat ggtttcatta tgtcgcgatg 660
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 agcaaactgt gccagcacc catgagaccc tctgaccac gtggaagatt gtggcggttca 1140

100120-000000

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 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
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Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

100120-606666

180												185												190											
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Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys																				
		210					215					220																							
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu																				
225					230					235																									
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe																				
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				260					265			270																							
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr																				
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Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys																				
						295					300																								
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr																				
305					310					315																									
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu																				
				325					330			335																							
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His																				
				340					345			350																							
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe																				
				355					360			365																							
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala																				
				370					375			380																							
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val																				
385					390					395																									
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr																				
				405					410			415																							
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys																				
				420					425			430																							
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro																				
				435					440			445																							
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile																				
				450					455			460																							

His Ala His Trp Val Leu Phe Leu Arg Asn
485 490

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

```
<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

```
<400> 134
agccaggatc gcagtaaaac tcc
```

```
<210> 135
<211> 50
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 135
attttaaactt gatgqgtctg cgtatcttga qtgcttacaa aaccttatct 50

```
<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens
```

<400> 136						
cccacgcgctc	cgctccgcgc	cctccccccc	gcctcccgctg	cggtccgctcg	gtggcctaga	60
gatgctgctg	ccgcggttgc	agttgtcgcg	cacgcctctg	cccgccagcc	cgctccaccg	120
ccgtagcgcc	cgagtgtcgg	ggggcgcacc	cgagtcgggg	catgaggccg	ggaaccgcgc	180
tacaggccgt	ctgctggcg	gtgctgctgg	gggggctgcg	ggccgcgacg	ggtcgctcgc	240
tgaqtgcctc	qqatttqqac	ctcagaggag	ggcagccagt	ctgccgggga	gggacacaga	300

```

<210> 137
<211> 382
<212> PRT
<213> Homo sapiens

<400> 137
Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
 1             5             10             15
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
             20             25             30
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
             35             40             45
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
 50             55             60
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
 65             70             75             80
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
             85             90             95
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
             100            105            110

```


Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<210> 138

F00120-20000000

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 138

gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 139

aagccaaaga agcctgcagg aggg 24

<210> 140

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 140

cagtccaagc ataaagggtcc tggc 24

<210> 141

<211> 1514

<212> DNA

<213> Homo sapiens

<400> 141

ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgagg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120
 ttgtgtttgc ctctgcagc ctcaaccgag agggcagcga gggcctacca ccatgatcac 180
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgactctg 240
 cctgcaccag cggcggggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
 gctgaccaag gtgggcatgc agcaaagtgt tgccctggga gagagactga ggaagaacta 600
 tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggctt ttattcgttc 660
 cactaacatt tttcggaatc tggagtcac ccgttggttg ctggctgggc ttttccagtg 720

000000-000000

```
<210> 142
<211> 428
<212> PRT
<213> Homo sapiens
```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 395 400
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
cttaaatttc agtcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

100720-200000

```
<210> 148
<211> 347
<212> PRT
<213> Homo sapiens
```

<400> 148																
Met	Ala	Leu	Leu	Phe	Ser	Leu	Ile	Leu	Ala	Ile	Cys	Thr	Arg	Pro	Gly	
1				5					10					15		
Phe	Leu	Ala	Ser	Pro	Ser	Gly	Val	Arg	Leu	Val	Gly	Gly	Leu	His	Arg	
			20					25					30			
Cys	Glu	Gly	Arg	Val	Glu	Val	Glu	Gln	Lys	Gly	Gln	Trp	Gly	Thr	Val	
		35					40					45				
Cys	Asp	Asp	Gly	Trp	Asp	Ile	Lys	Asp	Val	Ala	Val	Leu	Cys	Arg	Glu	
	50					55					60					
Leu	Gly	Cys	Gly	Ala	Ala	Ser	Gly	Thr	Pro	Ser	Gly	Ile	Leu	Tyr	Glu	
65					70					75					80	
Pro	Pro	Ala	Glu	Lys	Glu	Gln	Lys	Val	Leu	Ile	Gln	Ser	Val	Ser	Cys	
				85					90					95		
Thr	Gly	Thr	Glu	Asp	Thr	Leu	Ala	Gln	Cys	Glu	Gln	Glu	Glu	Val	Tyr	
			100					105					110			

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

100720-6062660

oligonucleotide probe

<400> 149

ttcagctcat caccttcacc tgcc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 150

ggctcataca aaataccact aggg

24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60
 acccacgcgt ccgcggacgc gtgggcggac gcgtgggccc gctaccagga agagtctgcc 120
 gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
 cctgggcgtc ttccgcctct tccggtgct gcagtgggtg cgcgggaagg cctacctgcg 240
 gaatgctgtg gtggtgatca caggcgccac ctccaggctg ggcaaagaat gtgcaaaagt 300
 cttctatgct gcgggtgcta aactggtgct ctgtggcccg aatggtgggg ccctagaaga 360
 gctcatcaga gaacttaccg cttctcatgc caccaagggt cagacacaca agccttactt 420
 ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
 tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
 catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
 gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780
 ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccacaccgc 840
 ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900
 ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tccctggctga 960
 cttactgcct tccttggtg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

F00120-00000000


```
<210> 153
<211> 310
<212> PRT
<213> Homo sapiens
```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

20

<211> 300
 <212> PRT
 <213> Homo sapiens

<400> 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val	1	5	10	15
Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys	20	25	30	
Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile	35	40	45	
Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val	50	55	60	
Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys	65	70	75	80
Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn	85	90	95	
Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly	100	105	110	
Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp	115	120	125	
Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn	130	135	140	
Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr	145	150	155	160
Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His	165	170	175	
Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	180	185	190	
Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile	195	200	205	
Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly	210	215	220	
Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu	225	230	235	240
Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met	245	250	255	

100720-206666

<400> 163
cccacgcgtc cgcgagcgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
tcagggagga qcaccgactg cgcgcacccc tqagaqatgg ttggtgccat gtggaaggtg 120

65				70				75				80				
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln	
				85					90					95		
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro	
				100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val	
				115					120					125		
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr	
				130					135					140		
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser	
				145					150					155		
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala	
				165					170					175		
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu	
				180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys	
				195					200					205		
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg	
				210					215					220		
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser	
				225					230					235		
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile	
				245					250					255		
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His	
				260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu	
				275					280					285		
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr	
				290					295					300		
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys	
				305					310					315		
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro	
				325					330					335		
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly	
				340					345					350		

cgaagggcttt	tccggctccg	gaatggcaca	tgtgggaatc	ccagtcttgt	tggctacaac	60
atttttccct	ttcctaacaa	gttctaacag	ctgttctaac	agctagtgat	caggggttct	120
tcttgctgga	gaagaaaggg	ctgagggcag	agcagggcac	tctcactcag	ggtgaccagc	180
tccttgcttc	tctgtggata	acagagcatg	agaaagtga	gagatgcagc	ggagtgaggt	240
gatggaagtc	taaaatagga	aggaattttg	tgtgcaatat	cagactctgg	gagcagttga	300
cctggagagc	ctgggggagg	gcctgcctaa	caagctttca	aaaaacagga	gcgacttcca	360
ctgggctggg	ataagacgtg	ccggtaggat	aggggaagact	gggttttagtc	ctaatatcaa	420
attgactggc	tgggtgaact	tcaacagcct	tttaacctct	ctgggagatg	aaaacgatgg	480
cttaaggggc	cagaaataga	gatgctttgt	aaaataaaat	tttaaaaaaa	gcaagtattt	540
tatagcataa	aggctagaga	cmetaataga	taacaggatt	ccctgaacat	tcctaagagag	600
gagaaagtat	gttaaaaata	gaaaacccaa	aatgcagaag	gaggagactc	acagagctaa	660
accaggatgg	ggaccttggg	tacggccagc	ctctttgtct	ctcccggaaa	ttatttttgg	720
tctgaccact	ctgccttgtg	ttttgcagaa	tcattgtgagg	gccaaccggg	gaaggtggag	780
cagatgagca	cacacaggag	ccgtctcctc	accgcgcgcc	ctctcagcat	ggaacagagg	840
cagccctggc	cccgggccct	ggaggtggac	agccgtctct	tggctctgct	ctcagtggtc	900
tgggtgctgc	tggccccccc	agcagccggc	atgcctcagt	tcagcacctt	ccactctgag	960
aatcgtgact	ggaccttcaa	ccacttgacc	gtccaccaag	ggacgggggc	cgtctatgtg	1020
ggggccatca	accgggtcta	taagctgaca	ggcaacctga	ccatccaggt	ggctcataag	1080
acagggccag	aagaggacaa	caagtctcgt	taccgcgcc	tcactgtgca	gcctgcagc	1140
gaagtgtcca	ccctcaccaa	caatgtcaac	aagctgctca	tcattgacta	ctctgagaac	1200
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<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

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20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
165 170 175

100120-20020000

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190
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 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
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 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
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 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255
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 260 265 270
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
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 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320
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 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
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 385 390 395 400
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
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 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
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 500 505 510
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
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<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171

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20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172

cttctgcctt ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

100-20-000000

<400> 173
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174
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<212> DNA
<213> Homo sapiens

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tgctggctcg cttgggcttc ctgggtgctc gcaggctgga ctggagcacc ctggtccttc 180
tgcggtcccg ccatcgacag ctggggctgc aggccaaagg ctggaacttc atgctggagg 240
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<211> 636

<213> Homo sapiens

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<221> MOD RES
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<223> Any amino acid

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20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

100120-202000

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ccctggtgag	ggttctctac	ttggccttcg	gtgggggtca	agacgcaggc	acctacgcca	120
aaggggagca	aagccgggct	cggcccagg	ccccaggac	ctccatctcc	caatgttggga	180
ggaatccgac	acgtgacgg	ctgtccgcg	tctcagacta	gaggagcgct	gtaaacgcca	240
tggctcccaa	gaagctgtcc	tgcttctggt	ccctgctgct	gccgctcagc	ctgacgctac	300
tgctgcccc	ggcagacact	cggtcgttcg	tagtggatag	gggtcatgac	cggtttctcc	360
tagacggggc	cccgttccgc	tatgtgtctg	gcagcctgca	ctactttcgg	gtaccgcggg	420


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<400> 177
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Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
      20             25             30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
      35             40             45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
      50             55             60

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Asp 65	Arg	Leu	Leu	Lys	Met 70	Arg	Trp	Ser	Gly	Leu 75	Asn	Ala	Ile	Gln	Phe 80
Tyr	Val	Pro	Trp	Asn 85	Tyr	His	Glu	Pro	Gln 90	Pro	Gly	Val	Tyr	Asn 95	Phe
Asn	Gly	Ser	Arg 100	Asp	Leu	Ile	Ala	Phe 105	Leu	Asn	Glu	Ala	Ala 110	Leu	Ala
Asn	Leu 115	Leu	Val	Ile	Leu	Arg	Pro 120	Gly	Pro	Tyr	Ile	Cys 125	Ala	Glu	Trp
Glu 130	Met	Gly	Gly	Leu	Pro	Ser 135	Trp	Leu	Leu	Arg	Lys 140	Pro	Glu	Ile	His
Leu 145	Arg	Thr	Ser	Asp 150	Pro	Asp	Phe	Leu	Ala 155	Ala	Val	Asp	Ser	Trp	Phe 160
Lys	Val	Leu	Leu 165	Pro	Lys	Ile	Tyr	Pro	Trp 170	Leu	Tyr	His	Asn 175	Gly	Gly
Asn	Ile	Ile	Ser 180	Ile	Gln	Val	Glu	Asn 185	Glu	Tyr	Gly	Ser	Tyr 190	Arg	Ala
Cys	Asp	Phe 195	Ser	Tyr	Met	Arg	His 200	Leu	Ala	Gly	Leu	Phe 205	Arg	Ala	Leu
Leu 210	Gly	Glu	Lys	Ile	Leu	Leu 215	Phe	Thr	Thr	Asp 220	Gly	Pro	Glu	Gly	Leu
Lys 225	Cys	Gly	Ser	Leu 230	Arg	Gly	Leu	Tyr	Thr 235	Thr	Val	Asp	Phe	Gly	Pro 240
Ala	Asp	Asn	Met 245	Thr	Lys	Ile	Phe	Thr 250	Leu	Leu	Arg	Lys	Tyr 255	Glu	Pro
His	Gly	Pro 260	Leu	Val	Asn	Ser	Glu	Tyr 265	Tyr	Thr	Gly	Trp	Leu 270	Asp	Tyr
Trp	Gly	Gln 275	Asn	His	Ser	Thr	Arg 280	Ser	Val	Ser	Ala	Val 285	Thr	Lys	Gly
Leu 290	Glu	Asn	Met	Leu	Lys	Leu 295	Gly	Ala	Ser	Val	Asn 300	Met	Tyr	Met	Phe
His 305	Gly	Gly	Thr	Asn 310	Phe	Gly	Tyr	Trp	Asn 315	Gly	Ala	Asp	Lys	Lys	Gly 320
Arg	Phe	Leu	Pro 325	Ile	Thr	Thr	Ser	Tyr 330	Asp	Tyr	Asp	Ala	Pro 335	Ile	Ser
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile

			340					345					350			
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro	
		355					360					365				
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu	
	370					375					380					
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu	
385					390					395					400	
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr	
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Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val	
			420					425					430			
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val	
		435					440					445				
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	450					455					460					
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465					470					475					480	
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				485					490					495		
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			500					505					510			
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Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu	
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Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
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<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

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<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

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<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180

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<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

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0903903-071004

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 183
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<212> DNA
<213> Homo sapiens
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aatattcttt	cgaaaaagtc	agagaagaga	gcagtttttag	tgacattcca	gatgtcaaaa	240	
acgattttgc	gttccttctt	cacatggtag	accagtatga	ccagctatat	tccaagcgtt	300	
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agtggacatt	tgaaaaactc	aggcagcaca	tttcacgcaa	cgcccaggac	aagcaggagt	420	
tgcactgtgtt	catgctgtcg	ggggtgcccg	atgctgtctt	tgacctcaca	gacctggatg	480	
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caaagttagt	cattcataat	gacggcacta	aactcttggt	actgaacagc	cttaagaaaa	900	
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aaattgttac	tattctctccc	tctattacc	atgtcaaaaa	cttggagtc	ctttatttct	1140	
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tagatgtgag	ctacaacaac	atttcaatga	tccaataga	aataggattg	cttcagaacc	1260	
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<210> 185
<211> 501
<212> PRT
<213> Homo sapiens
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<400> 185															
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Cys	Val	Tyr	Gly 20	Phe	Ile	Cys	Leu	Tyr 25	Thr	Leu	Phe	Trp	Leu 30	Phe	Arg
Ile	Pro	Leu 35	Lys	Glu	Tyr	Ser	Phe 40	Glu	Lys	Val	Arg	Glu 45	Glu	Ser	Ser
Phe 50	Ser	Asp	Ile	Pro	Asp	Val 55	Lys	Asn	Asp	Phe	Ala 60	Phe	Leu	Leu	His
Met 65	Val	Asp	Gln	Tyr	Asp 70	Gln	Leu	Tyr	Ser	Lys 75	Arg	Phe	Gly	Val	Phe 80
Leu	Ser	Glu	Val	Ser 85	Glu	Asn	Lys	Leu	Arg 90	Glu	Ile	Ser	Leu	Asn 95	His
Glu	Trp	Thr	Phe 100	Glu	Lys	Leu	Arg	Gln 105	His	Ile	Ser	Arg	Asn 110	Ala	Gln
Asp	Lys	Gln 115	Glu	Leu	His	Leu 120	Phe	Met	Leu	Ser	Gly 125	Val	Pro	Asp	Ala
Val 130	Phe	Asp	Leu	Thr	Asp 135	Leu	Asp	Val	Leu	Lys	Leu 140	Glu	Leu	Ile	Pro
Glu 145	Ala	Lys	Ile	Pro	Ala 150	Lys	Ile	Ser	Gln	Met 155	Thr	Asn	Leu	Gln	Glu 160
Leu	His	Leu	Cys	His 165	Cys	Pro	Ala	Lys	Val 170	Glu	Gln	Thr	Ala	Phe 175	Ser
Phe	Leu	Arg	Asp 180	His	Leu	Arg	Cys	Leu 185	His	Val	Lys	Phe	Thr 190	Asp	Val

Ala	Glu	Ile	Pro	Ala	Trp	Val	Tyr	Leu	Leu	Lys	Asn	Leu	Arg	Glu	Leu
195						200						205			
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210						215						220			
Glu	Ser	Leu	Arg	Glu	Leu	Arg	His	Leu	Lys	Ile	Leu	His	Val	Lys	Ser
225						230						240			
Asn	Leu	Thr	Lys	Val	Pro	Ser	Asn	Ile	Thr	Asp	Val	Ala	Pro	His	Leu
			245						250			255			
Thr	Lys	Leu	Val	Ile	His	Asn	Asp	Gly	Thr	Lys	Leu	Leu	Val	Leu	Asn
			260						265			270			
Ser	Leu	Lys	Lys	Met	Met	Asn	Val	Ala	Glu	Leu	Glu	Leu	Gln	Asn	Cys
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Glu	Leu	Glu	Arg	Ile	Pro	His	Ala	Ile	Phe	Ser	Leu	Ser	Asn	Leu	Gln
290						295						300			
Glu	Leu	Asp	Leu	Lys	Ser	Asn	Asn	Ile	Arg	Thr	Ile	Glu	Glu	Ile	Ile
305						310						320			
Ser	Phe	Gln	His	Leu	Lys	Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	His	Asn
			325						330			335			
Lys	Ile	Val	Thr	Ile	Pro	Pro	Ser	Ile	Thr	His	Val	Lys	Asn	Leu	Glu
			340						345			350			
Ser	Leu	Tyr	Phe	Ser	Asn	Asn	Lys	Leu	Glu	Ser	Leu	Pro	Val	Ala	Val
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Phe	Ser	Leu	Gln	Lys	Leu	Arg	Cys	Leu	Asp	Val	Ser	Tyr	Asn	Asn	Ile
370						375						380			
Ser	Met	Ile	Pro	Ile	Glu	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	His	Leu
385						390						395			
His	Ile	Thr	Gly	Asn	Lys	Val	Asp	Ile	Leu	Pro	Lys	Gln	Leu	Phe	Lys
			405						410			415			
Cys	Ile	Lys	Leu	Arg	Thr	Leu	Asn	Leu	Gly	Gln	Asn	Cys	Ile	Thr	Ser
			420						425			430			
Leu	Pro	Glu	Lys	Val	Gly	Gln	Leu	Ser	Gln	Leu	Thr	Gln	Leu	Glu	Leu
435						440						445			
Lys	Gly	Asn	Cys	Leu	Asp	Arg	Leu	Pro	Ala	Gln	Leu	Gly	Gln	Cys	Arg
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aagacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tcttcccttg 180
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 atcgctgggt gctatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360
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 cacaaccag acaaggtgtg gtggggccaag aacagccagg ccaaaaccat tgccacggag 480
 tcttgctctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540
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 aatatggcag agaccacaaa agccatgac ctgcaactca atcccagtg gaactgcacc 1140
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<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

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			20					25					30		
Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	Lys	Ala	Met
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Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg
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Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu	Asp
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Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr
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Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp	Tyr
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Val	Pro	Val	Phe	Glu	Ser	Ser	Ser	Ser	Thr	Leu	Thr	Phe	Gln	Ile	Val
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Phe	Ser	Pro	Asn	Ile	Ser	Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr
145					150					155					160
Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu
				165					170					175	
Leu	Ala	Tyr	Cys	Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys	Ile
			180					185					190		
Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys
		195					200					205			
Phe	Asp	Phe	Leu	Ala	Ile	Tyr	Asp	Gly	Pro	Ser	Thr	Asn	Ser	Gly	Leu
	210					215					220				
Ile	Gly	Gln	Val	Cys	Gly	Arg	Val	Thr	Pro	Thr	Phe	Glu	Ser	Ser	Ser
225					230					235					240
Asn	Ser	Leu	Thr	Val	Val	Leu	Ser	Thr	Asp	Tyr	Ala	Asn	Ser	Tyr	Arg
				245					250					255	
Gly	Phe	Ser	Ala	Ser	Tyr	Thr	Ser	Ile	Tyr	Ala	Glu	Asn	Ile	Asn	Thr
			260					265					270		
Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys
		275					280					285			

Ser	Tyr	Leu	Glu	Ala	Phe	Asn	Ser	Asn	Gly	Asn	Asn	Leu	Gln	Leu	Lys
290						295				300					
Asp	Pro	Thr	Cys	Arg	Pro	Lys	Leu	Ser	Asn	Val	Val	Glu	Phe	Ser	Val
305				310					315						320
Pro	Leu	Asn	Gly	Cys	Gly	Thr	Ile	Arg	Lys	Val	Glu	Asp	Gln	Ser	Ile
			325					330						335	
Thr	Tyr	Thr	Asn	Ile	Ile	Thr	Phe	Ser	Ala	Ser	Ser	Thr	Ser	Glu	Val
			340				345						350		
Ile	Thr	Arg	Gln	Lys	Gln	Leu	Gln	Ile	Ile	Val	Lys	Cys	Glu	Met	Gly
		355					360					365			
His	Asn	Ser	Thr	Val	Glu	Ile	Ile	Tyr	Ile	Thr	Glu	Asp	Asp	Val	Ile
	370					375					380				
Gln	Ser	Gln	Asn	Ala	Leu	Gly	Lys	Tyr	Asn	Thr	Ser	Met	Ala	Leu	Phe
385					390					395					400
Glu	Ser	Asn	Ser	Phe	Glu	Lys	Thr	Ile	Leu	Glu	Ser	Pro	Tyr	Tyr	Val
				405					410					415	
Asp	Leu	Asn	Gln	Thr	Leu	Phe	Val	Gln	Val	Ser	Leu	His	Thr	Ser	Asp
			420					425					430		
Pro	Asn	Leu	Val	Val	Phe	Leu	Asp	Thr	Cys	Arg	Ala	Ser	Pro	Thr	Ser
		435					440					445			
Asp	Phe	Ala	Ser	Pro	Thr	Tyr	Asp	Leu	Ile	Lys	Ser	Gly	Cys	Ser	Arg
	450					455					460				
Asp	Glu	Thr	Cys	Lys	Val	Tyr	Pro	Leu	Phe	Gly	His	Tyr	Gly	Arg	Phe
465					470					475					480
Gln	Phe	Asn	Ala	Phe	Lys	Phe	Leu	Arg	Ser	Met	Ser	Ser	Val	Tyr	Leu
				485					490					495	
Gln	Cys	Lys	Val	Leu	Ile	Cys	Asp	Ser	Ser	Asp	His	Gln	Ser	Arg	Cys
			500					505					510		
Asn	Gln	Gly	Cys	Val	Ser	Arg	Ser	Lys	Arg	Asp	Ile	Ser	Ser	Tyr	Lys
		515					520					525			
Trp	Lys	Thr	Asp	Ser	Ile	Ile	Gly	Pro	Ile	Arg	Leu	Lys	Arg	Asp	Arg
	530					535					540				
Ser	Ala	Ser	Gly	Asn	Ser	Gly	Phe	Gln	His	Glu	Thr	His	Ala	Glu	Glu
545					550					555					560
Thr	Pro	Asn	Gln	Pro	Phe	Asn	Ser	Val	His	Leu	Phe	Ser	Phe	Met	Val

	565		570		575										
Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala	Thr	Ile	Thr	Val	Arg	His	Phe
	580							585					590		
Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr	
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<210> 191
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 191
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<210> 192
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 192
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<210> 193
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 193
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<210> 194
 <211> 2362
 <212> DNA
 <213> Homo sapiens

<400> 194
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100720-034004

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<210> 195
<211> 467
<212> PRT
<213> Homo sapiens
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20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
35 40 45

Trp	Phe	Asp	Gln	Ala	Lys	Phe	Gly	Ile	Phe	Ile	His	Trp	Gly	Val	Phe
50						55					60				
Ser	Val	Pro	Ser	Phe	Gly	Ser	Glu	Trp	Phe	Trp	Trp	Tyr	Trp	Gln	Lys
65					70					75					80
Glu	Lys	Ile	Pro	Lys	Tyr	Val	Glu	Phe	Met	Lys	Asp	Asn	Tyr	Pro	Pro
				85					90					95	
Ser	Phe	Lys	Tyr	Glu	Asp	Phe	Gly	Pro	Leu	Phe	Thr	Ala	Lys	Phe	Phe
			100					105					110		
Asn	Ala	Asn	Gln	Trp	Ala	Asp	Ile	Phe	Gln	Ala	Ser	Gly	Ala	Lys	Tyr
		115					120					125			
Ile	Val	Leu	Thr	Ser	Lys	His	His	Glu	Gly	Phe	Thr	Leu	Trp	Gly	Ser
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Glu	Tyr	Ser	Trp	Asn	Trp	Asn	Ala	Ile	Asp	Glu	Gly	Pro	Lys	Arg	Asp
145					150					155					160
Ile	Val	Lys	Glu	Leu	Glu	Val	Ala	Ile	Arg	Asn	Arg	Thr	Asp	Leu	Arg
				165					170					175	
Phe	Gly	Leu	Tyr	Tyr	Ser	Leu	Phe	Glu	Trp	Phe	His	Pro	Leu	Phe	Leu
			180					185					190		
Glu	Asp	Glu	Ser	Ser	Ser	Phe	His	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys
		195					200					205			
Thr	Leu	Pro	Glu	Leu	Tyr	Glu	Leu	Val	Asn	Asn	Tyr	Gln	Pro	Glu	Val
	210					215					220				
Leu	Trp	Ser	Asp	Gly	Asp	Gly	Gly	Ala	Pro	Asp	Gln	Tyr	Trp	Asn	Ser
225					230					235					240
Thr	Gly	Phe	Leu	Ala	Trp	Leu	Tyr	Asn	Glu	Ser	Pro	Val	Arg	Gly	Thr
				245					250					255	
Val	Val	Thr	Asn	Asp	Arg	Trp	Gly	Ala	Gly	Ser	Ile	Cys	Lys	His	Gly
			260					265					270		
Gly	Phe	Tyr	Thr	Cys	Ser	Asp	Arg	Tyr	Asn	Pro	Gly	His	Leu	Leu	Pro
		275					280					285			
His	Lys	Trp	Glu	Asn	Cys	Met	Thr	Ile	Asp	Lys	Leu	Ser	Trp	Gly	Tyr
	290					295					300				
Arg	Arg	Glu	Ala	Gly	Ile	Ser	Asp	Tyr	Leu	Thr	Ile	Glu	Glu	Leu	Val
305					310					315					320
Lys	Gln	Leu	Val	Glu	Thr	Val	Ser	Cys	Gly	Gly	Asn	Leu	Leu	Met	Asn
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<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 198

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24

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 199

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45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

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```

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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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```

```

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20             25             30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35             40             45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50             55             60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65             70             75             80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85             90             95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
      100            105            110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
      115            120            125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
      130            135            140

```

100720-200000

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
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 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
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 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
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 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

100120-00000000

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gtcagtgaca gtacctactc gg

22

<211> 24

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

tggagcagga ggagtagtag tagg

24

<211> 50

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<211> 1620

<212> DNA

<213> Homo sapiens

<221> modified_base

<222> (973)

<223> a, t, c or g

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<221> modified_base
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<222> (977)

<223> a, t, c or g

<221> modified base

<222> (996)

<223> a, t, c or g

<221> modified base

<222> (1003)

<223> a, t, c or g

<400> 206

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```

<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

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Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
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Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
      20              25              30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
      35              40              45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
      50              55              60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
      65              70              75              80

```

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
 260 265 270
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
 275 280 285
 Asp Gly Glu Asn Lys Lys Asp Lys
 290 295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 208

gcttgatat tcgcatgggc ctac

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 209
 tggagacaat atccctgagg

20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 210
 aacagttggc cacagcatgg cagg

24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 211
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag

50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212

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 caacagcgcc aacgaccaga acctaggcaa cgggtcatggc aaagacctcc ttaatggagt 240
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 cctgccctgc cgctaccgct acgagccggc cctgggtctcc ccgcggcggtg tgcgtgtcaa 360
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100120-2062060

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
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Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

100120-20000000

115					120					125								
Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr			
130					135					140								
Arg	Cys	Glu	Val	Ile	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu			
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Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg			
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Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala			
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Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly			
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Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr			
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Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Gly	Leu	Ala	Pro			
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Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Lys	Gly	Arg	Val	Tyr	Tyr	Leu	Glu			
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His	Pro	Glu	Lys	Leu	Thr	Leu	Thr	Glu	Ala	Arg	Glu	Ala	Cys	Gln	Glu			
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Asp	Asp	Ala	Thr	Ile	Ala	Lys	Val	Gly	Gln	Leu	Phe	Ala	Ala	Trp	Lys			
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Phe	His	Gly	Leu	Asp	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser			
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Val	Arg	Tyr	Pro	Val	Val	His	Pro	His	Pro	Asn	Cys	Gly	Pro	Pro	Glu			
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Pro	Gly	Val	Arg	Ser	Phe	Gly	Phe	Pro	Asp	Pro	Gln	Ser	Arg	Leu	Tyr			
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Gly	Val	Tyr	Cys	Tyr	Arg	Gln	His											
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<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 215

ttcccttgtg gggtggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217

agccagtgag gaaatgag

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

000000-000000

<210> 219

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 219

gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 220

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aaa 1503

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<210> 221

<211> 328

<212> PRT

<213> Homo sapiens

<400> 221

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

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Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

100120-0000000

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
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<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

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20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

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23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

100120-606060

<400> 225
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44

<210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens

<400> 226
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 gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040
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Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
          35           40           45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
          50           55           60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
          65           70           75           80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
          85           90           95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
          100          105          110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
          115          120          125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
          130          135          140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
          145          150          155          160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
          165          170          175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
          180          185          190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
          195          200          205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
          210          215          220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
          225          230          235          240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
          245          250          255

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Thr	Val	Asp	Ala	Gly	Val	Arg	Lys	Gly	Ile	Pro	Lys	Val	Val	Val	Val
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Phe	Ile	Asp	Gly	Trp	Pro	Ser	Asp	Asp	Ile	Glu	Glu	Ala	Gly	Ile	Val
		275				280						285			
Ala	Arg	Glu	Phe	Gly	Val	Asn	Val	Phe	Ile	Val	Ser	Val	Ala	Lys	Pro
		290				295				300					
Ile	Pro	Glu	Glu	Leu	Gly	Met	Val	Gln	Asp	Val	Thr	Phe	Val	Asp	Lys
305				310				315						320	
Ala	Val	Cys	Arg	Asn	Asn	Gly	Phe	Phe	Ser	Tyr	His	Met	Pro	Asn	Trp
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Phe	Gly	Thr	Thr	Lys	Tyr	Val	Lys	Pro	Leu	Val	Gln	Lys	Leu	Cys	Thr
		340						345				350			
His	Glu	Gln	Met	Met	Cys	Ser	Lys	Thr	Cys	Tyr	Asn	Ser	Val	Asn	Ile
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Ala	Phe	Leu	Ile	Asp	Gly	Ser	Ser	Ser	Val	Gly	Asp	Ser	Asn	Phe	Arg
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Leu	Met	Leu	Glu	Phe	Val	Ser	Asn	Ile	Ala	Lys	Thr	Phe	Glu	Ile	Ser
385				390				395						400	
Asp	Ile	Gly	Ala	Lys	Ile	Ala	Ala	Val	Gln	Phe	Thr	Tyr	Asp	Gln	Arg
				405				410						415	
Thr	Glu	Phe	Ser	Phe	Thr	Asp	Tyr	Ser	Thr	Lys	Glu	Asn	Val	Leu	Ala
		420						425				430			
Val	Ile	Arg	Asn	Ile	Arg	Tyr	Met	Ser	Gly	Gly	Thr	Ala	Thr	Gly	Asp
		435				440						445			
Ala	Ile	Ser	Phe	Thr	Val	Arg	Asn	Val	Phe	Gly	Pro	Ile	Arg	Glu	Ser
		450				455				460					
Pro	Asn	Lys	Asn	Phe	Leu	Val	Ile	Val	Thr	Asp	Gly	Gln	Ser	Tyr	Asp
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Asp	Val	Gln	Gly	Pro	Ala	Ala	Ala	Ala	His	Asp	Ala	Gly	Ile	Thr	Ile
				485				490						495	
Phe	Ser	Val	Gly	Val	Ala	Trp	Ala	Pro	Leu	Asp	Asp	Leu	Lys	Asp	Met
		500						505				510			
Ala	Ser	Lys	Pro	Lys	Glu	Ser	His	Ala	Phe	Phe	Thr	Arg	Glu	Phe	Thr
		515				520						525			
Gly	Leu	Glu	Pro	Ile	Val	Ser	Asp	Val	Ile	Arg	Gly	Ile	Cys	Arg	Asp
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<210> 228
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<212> DNA
<213> Artificial Sequence
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<400> 228
tgggtctcgca caccgatc 18
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229
ctgctgtcca cagggggag 18

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<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaagca tactgctc 18

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<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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gagatagcaa tttccgcc 18

<210> 232

<400> 235						
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gcctgctgct	ggcgggcgcg	gtccccacgg	cccccgcgcc	cgctccgacg	gcgacctcgg	240
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acgaggactg	tgggcccagc	atgtactgac	aggttgcgag	cttccagtac	acctgccacg	660
catgccqqqq	ccgaaggaat	ctctgcaccc	gggacagtga	gtgctgtgga	gaccagctgt	720

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
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Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
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<210> 237

F00740-EBE00000

<211> 17
 <212> DNA
 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

 <400> 237
 ggagctgcac cccttgc 17

 <210> 238
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

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 <210> 239
 <211> 24
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 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 239
 gcagagcggg gatgcagcgg cttg 24

 <210> 240
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 240
 ttggcagctt catggagg 18

 <210> 241
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 241
 cctgggcaaa aatgcaac 18

100120-000000

<210> 242
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<400> 242
 ctccagctcc tggcgcacct cctc

24

<210> 243
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 243
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45

<210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

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 cacacataca ccttcctctc cttcactgaa gactcacagt cactcactct 200
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggctggcc 250
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 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

100120-20220000

F

姓名	性别	年龄	职业	住址	电话	备注
王德胜	男	45	工人	XX路XX号	XXXX	
李秀英	女	38	教师	XX街XX号	XXXX	
张国强	男	52	干部	XX巷XX号	XXXX	
刘小红	女	28	学生	XX村XX组	XXXX	
陈大伟	男	35	医生	XX路XX号	XXXX	
赵小芳	女	42	护士	XX街XX号	XXXX	
孙志明	男	58	农民	XX村XX组	XXXX	
周丽娟	女	32	会计	XX路XX号	XXXX	
吴建刚	男	48	工程师	XX街XX号	XXXX	
郑晓燕	女	25	记者	XX巷XX号	XXXX	
冯大刚	男	55	工人	XX村XX组	XXXX	
马小梅	女	30	教师	XX路XX号	XXXX	
徐志强	男	40	干部	XX街XX号	XXXX	
黄丽娟	女	35	学生	XX巷XX号	XXXX	
郭大伟	男	50	医生	XX村XX组	XXXX	
李秀英	女	45	护士	XX路XX号	XXXX	
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孙志明	男	58	干部	XX街XX号	XXXX	
周丽娟	女	32	学生	XX巷XX号	XXXX	
吴建刚	男	48	医生	XX村XX组	XXXX	
郑晓燕	女	25	护士	XX路XX号	XXXX	
冯大刚	男	55	会计	XX街XX号	XXXX	
马小梅	女	30	记者	XX巷XX号	XXXX	
徐志强	男	40	工人	XX村XX组	XXXX	
黄丽娟	女	35	教师	XX路XX号	XXXX	
郭大伟	男	50	干部	XX街XX号	XXXX	
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周丽娟	女	32	教师	XX路XX号	XXXX	
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吴建刚	男	48	会计	XX街XX号	XXXX	
郑晓燕	女	25	记者	XX巷XX号	XXXX	
冯大刚	男	55	工人	XX村XX组	XXXX	
马小梅	女	30				

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<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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				20					25					30
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
				35					40					45
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
				50					55					60
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
				65					70					75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
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Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
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Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
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Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
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Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
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F00120-206660

Asn	Gln	Leu	Tyr	Arg 155	Ile	Ala	Pro	Arg	Ala 160	Phe	Ser	Gly	Leu	Ser 165
Asn	Leu	Leu	Arg	Leu 170	His	Leu	Asn	Ser	Asn 175	Leu	Leu	Arg	Ala	Ile 180
Asp	Ser	Arg	Trp	Phe 185	Glu	Met	Leu	Pro	Asn 190	Leu	Glu	Ile	Leu	Met 195
Ile	Gly	Gly	Asn	Lys 200	Val	Asp	Ala	Ile	Leu 205	Asp	Met	Asn	Phe	Arg 210
Pro	Leu	Ala	Asn	Leu 215	Arg	Ser	Leu	Val	Leu 220	Ala	Gly	Met	Asn	Leu 225
Arg	Glu	Ile	Ser	Asp 230	Tyr	Ala	Leu	Glu	Gly 235	Leu	Gln	Ser	Leu	Glu 240
Ser	Leu	Ser	Phe	Tyr 245	Asp	Asn	Gln	Leu	Ala 250	Arg	Val	Pro	Arg	Arg 255
Ala	Leu	Glu	Gln	Val 260	Pro	Gly	Leu	Lys	Phe 265	Leu	Asp	Leu	Asn	Lys 270
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His	Leu	Lys	Glu	Leu 290	Gly	Leu	Asn	Asn	Met 295	Glu	Glu	Leu	Val	Ser 300
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Phe	His	His	Leu	Pro 335	Gln	Met	Glu	Thr	Leu 340	Met	Leu	Asn	Asn	Asn 345
Ala	Leu	Ser	Ala	Leu 350	His	Gln	Gln	Thr	Val 355	Glu	Ser	Leu	Pro	Asn 360
Leu	Gln	Glu	Val	Gly 365	Leu	His	Gly	Asn	Pro 370	Ile	Arg	Cys	Asp	Cys 375
Val	Ile	Arg	Trp	Ala 380	Asn	Ala	Thr	Gly	Thr 385	Arg	Val	Arg	Phe	Ile 390
Glu	Pro	Gln	Ser	Thr 395	Leu	Cys	Ala	Glu	Pro 400	Pro	Asp	Leu	Gln	Arg 405
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys

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Ala Ser Gly Glu Ser Met Val Leu His	Cys Arg Ala Leu Ala Glu				
440	445	450			
Pro Glu Pro Glu Ile Tyr Trp Val Thr	Pro Ala Gly Leu Arg Leu				
455	460	465			
Thr Pro Ala His Ala Gly Arg Arg Tyr	Arg Val Tyr Pro Glu Gly				
470	475	480			
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Phe Ala Asp Ala His Thr Gln Leu Ala	Cys Val Trp Ala Arg Thr				
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Lys Glu Ala Thr Ser Cys His Arg Ala	Leu Gly Asp Arg Pro Gly				
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Gly Arg Arg Pro Leu Pro Pro Ala Trp	Ala Phe Trp Gly Trp Ser				
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<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg	35	40	45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe	50	55	60	
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr	65	70	75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu	80	85	90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys				

100120-6062060

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Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro
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Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu
				125					130					135
Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp
				140					145					150
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu
				155					160					165
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp
				170					175					180
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val
				185					190					195
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu
				200					205					210
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala
				215					220					225
Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp
				230					235					240
Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu
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Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu
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Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp
				290					295					300
Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr
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Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr
				320					325					330
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser
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 395 400 405
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 410 415 420
 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe
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 470 475 480
 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile
 485 490 495
 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly
 500 505 510
 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp
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<212> DNA

<213> Artificial Sequence

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<400> 252

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<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

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<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

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<211> 452

<212> PRT

<213> Homo Sapien

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				20					25				30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35					40				45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	50	55	60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	65	70	75
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Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	140	145	150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	155	160	165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	170	175	180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	185	190	195
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Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	245	250	255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	260	265	270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	275	280	285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	290	295	300
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100120-6062000

Gln Glu

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<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

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				20					25					30

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
				35					40					45

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
				50					55					60

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
				65					70					75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
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100740-005555

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<211> 2427
<212> DNA
<213> Homo Sapien

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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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				20					25					30
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Glu	Leu	Ser	Leu	Thr 50	Phe	Ala	Leu	Arg	Gln 55	Gln	Asn	Val	Glu	Arg 60
Leu	Ser	Glu	Leu	Val 65	Gln	Ala	Val	Ser	Asp 70	Pro	Ser	Ser	Pro	Gln 75
Tyr	Gly	Lys	Tyr	Leu 80	Thr	Leu	Glu	Asn	Val 85	Ala	Asp	Leu	Val	Arg 90
Pro	Ser	Pro	Leu	Thr 95	Leu	His	Thr	Val	Gln 100	Lys	Trp	Leu	Leu	Ala 105
Ala	Gly	Ala	Gln	Lys 110	Cys	His	Ser	Val	Ile 115	Thr	Gln	Asp	Phe	Leu 120
Thr	Cys	Trp	Leu	Ser 125	Ile	Arg	Gln	Ala	Glu 130	Leu	Leu	Leu	Pro	Gly 135
Ala	Glu	Phe	His	His 140	Tyr	Val	Gly	Gly	Pro 145	Thr	Glu	Thr	His	Val 150
Val	Arg	Ser	Pro	His 155	Pro	Tyr	Gln	Leu	Pro 160	Gln	Ala	Leu	Ala	Pro 165
His	Val	Asp	Phe	Val 170	Gly	Gly	Leu	His	Arg 175	Phe	Pro	Pro	Thr	Ser 180
Ser	Leu	Arg	Gln	Arg 185	Pro	Glu	Pro	Gln	Val 190	Thr	Gly	Thr	Val	Gly 195
Leu	His	Leu	Gly	Val 200	Thr	Pro	Ser	Val	Ile 205	Arg	Lys	Arg	Tyr	Asn 210
Leu	Thr	Ser	Gln	Asp 215	Val	Gly	Ser	Gly	Thr 220	Ser	Asn	Asn	Ser	Gln 225
Ala	Cys	Ala	Gln	Phe 230	Leu	Glu	Gln	Tyr	Phe 235	His	Asp	Ser	Asp	Leu 240
Ala	Gln	Phe	Met	Arg 245	Leu	Phe	Gly	Gly	Asn 250	Phe	Ala	His	Gln	Ala 255
Ser	Val	Ala	Arg	Val 260	Val	Gly	Gln	Gln	Gly 265	Arg	Gly	Arg	Ala	Gly 270
Ile	Glu	Ala	Ser	Leu 275	Asp	Val	Gln	Tyr	Leu 280	Met	Ser	Ala	Gly	Ala 285

Asn Ile Ser Thr	Trp Val Tyr Ser Ser	Pro Gly Arg His Glu Gly	290	295	300
Gln Glu Pro Phe	Leu Gln Trp Leu Met	Leu Leu Ser Asn Glu Ser	305	310	315
Ala Leu Pro His	Val His Thr Val Ser	Tyr Gly Asp Asp Glu Asp	320	325	330
Ser Leu Ser Ser	Ala Tyr Ile Gln Arg	Val Asn Thr Glu Leu Met	335	340	345
Lys Ala Ala Ala	Arg Gly Leu Thr Leu	Leu Phe Ala Ser Gly Asp	350	355	360
Ser Gly Ala Gly	Cys Trp Ser Val Ser	Gly Arg His Gln Phe Arg	365	370	375
Pro Thr Phe Pro	Ala Ser Ser Pro Tyr	Val Thr Thr Val Gly Gly	380	385	390
Thr Ser Phe Gln	Glu Pro Phe Leu Ile	Thr Asn Glu Ile Val Asp	395	400	405
Tyr Ile Ser Gly	Gly Gly Phe Ser Asn	Val Phe Pro Arg Pro Ser	410	415	420
Tyr Gln Glu Glu	Ala Val Thr Lys Phe	Leu Ser Ser Ser Pro His	425	430	435
Leu Pro Pro Ser	Ser Tyr Phe Asn Ala	Ser Gly Arg Ala Tyr Pro	440	445	450
Asp Val Ala Ala	Leu Ser Asp Gly Tyr	Trp Val Val Ser Asn Arg	455	460	465
Val Pro Ile Pro	Trp Val Ser Gly Thr	Ser Ala Ser Thr Pro Val	470	475	480
Phe Gly Gly Ile	Leu Ser Leu Ile Asn	Glu His Arg Ile Leu Ser	485	490	495
Gly Arg Pro Pro	Leu Gly Phe Leu Asn	Pro Arg Leu Tyr Gln Gln	500	505	510
His Gly Ala Gly	Leu Phe Asp Val Thr	Arg Gly Cys His Glu Ser	515	520	525
Cys Leu Asp Glu	Glu Val Glu Gly Gln	Gly Phe Cys Ser Gly Pro	530	535	540
Gly Trp Asp Pro	Val Thr Gly Trp Gly	Thr Pro Thr Ser Gln Leu	545	550	555

FOOT-20-00000000

Cys

<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

<400> 260

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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

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Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	35	40	45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	50	55	60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	65	70	75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	80	85	90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	95	100	105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	110	115	120	

090909-031004

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Arg Phe Ser Ile	Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val	Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His	Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val	Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe	Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro	Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val	Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp	Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys	Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly	Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn	Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu	Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly	Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg	Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn	Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp	Cys Arg Glu Gly	380		

100120-000000

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tgg	ac	ggcgc	ctgg	ctgctg	gccggcatca	tcagctgggg	cgagggctgt	850
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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

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Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

100120-6052050

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
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Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
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Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
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<212> DNA

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<210> 266

<211> 24

100120-202050

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F00120-20020000

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<210> 281

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<211> 1875

<212> DNA

<213> Homo Sapien

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<212> PRT
<213> Homo Sapien
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Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
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Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
				50					55					60
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
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Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe
				80					85					90
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
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Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
				110					115					120
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
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Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
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 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
 185 190 195
 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
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 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
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 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
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 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
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 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
 305 310 315
 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
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 335 340 345
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
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 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
 365 370 375
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 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
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100120-2062000

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
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Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
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 <212> DNA
 <213> Homo Sapien

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090909-074004

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<212> PRT
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Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	35	40	45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	50	55	60
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	65	70	75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	80	85	90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	95	100	105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser			

100740-2062000

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Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala	335		340		345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn	350		355		360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys	365		370		375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys	380		385		390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln	395		400		405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly	410		415		420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp	425		430		435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala	440		445		450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser	455		460		465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu	470		475		480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln	485		490		495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu	500		505		510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn	515		520		525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn	530		535		540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg	545		550		555

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Ala	Ala	Arg	Glu	Arg 590	Arg	Met	His	Val	Met 595	Pro	Glu	Asp	Asp	Val 600
Phe	Phe	Ile	Val	Asp 605	Val	Lys	Ile	Glu	Asp 610	Ile	Gly	Val	Tyr	Ser 615
Cys	Thr	Ala	Gln	Asn 620	Ser	Ala	Gly	Ser	Ile 625	Ser	Ala	Asn	Ala	Thr 630
Leu	Thr	Val	Leu	Glu 635	Thr	Pro	Ser	Phe	Leu 640	Arg	Pro	Leu	Leu	Asp 645
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Gly	Gly	Ser	Pro	Pro 665	Pro	Lys	Leu	Asn	Trp 670	Thr	Lys	Asp	Asp	Ser 675
Pro	Leu	Val	Val	Thr 680	Glu	Arg	His	Phe	Phe 685	Ala	Ala	Gly	Asn	Gln 690
Leu	Leu	Ile	Ile	Val 695	Asp	Ser	Asp	Val	Ser 700	Asp	Ala	Gly	Lys	Tyr 705
Thr	Cys	Glu	Met	Ser 710	Asn	Thr	Leu	Gly	Thr 715	Glu	Arg	Gly	Asn	Val 720
Arg	Leu	Ser	Val	Ile 725	Pro	Thr	Pro	Thr	Cys 730	Asp	Ser	Pro	Gln	Met 735
Thr	Ala	Pro	Ser	Leu 740	Asp	Asp	Asp	Gly	Trp 745	Ala	Thr	Val	Gly	Val 750
Val	Ile	Ile	Ala	Val 755	Val	Cys	Cys	Val	Val 760	Gly	Thr	Ser	Leu	Val 765
Trp	Val	Val	Ile	Ile 770	Tyr	His	Thr	Arg	Arg 775	Arg	Asn	Glu	Asp	Cys 780
Ser	Ile	Thr	Asn	Thr 785	Asp	Glu	Thr	Asn	Leu 790	Pro	Ala	Asp	Ile	Pro 795
Ser	Tyr	Leu	Ser	Ser 800	Gln	Gly	Thr	Leu	Ala 805	Asp	Arg	Gln	Asp	Gly 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
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 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
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 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
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 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
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 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
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 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
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 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
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 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
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 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
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 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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<211> 2906

100720-2052550

<212> DNA

<213> Homo Sapien

<400> 291

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<210> 292
<211> 640
<212> PRT
<213> Homo Sapien
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				20					25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

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Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly					
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Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly					
	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg					
	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp					
	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln					
	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile					
	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val					
	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp					
	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His					
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Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys					
	320		325		330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp					
	335		340		345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro					
	350		355		360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys					
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Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn					
	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val					
	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp					
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100120-000000

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
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 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
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 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
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 485 490 495
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
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 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
 515 520 525
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
 530 535 540
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
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 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
 560 565 570
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 575 580 585
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
 590 595 600
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
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0990003-071004

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<213> Homo Sapien

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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
65 70 75

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Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
                        80                        85                        90
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Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
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Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

				215					220					225
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala
				230					235					240
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met
				245					250					255
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu
				260					265					270
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly
				275					280					285
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn
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Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu
				305					310					315
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser
				320					325					330
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn
				335					340					345
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser
				350					355					360
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile
				365					370					375
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg
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Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala
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Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn
				410					415					420
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys
				425					430					435
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys
				440					445					450
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln
				455					460					465
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly
				470					475					480

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Phe Pro Lys Pro	Gln Ile Thr Val Gln	Pro Glu Thr Gln Ser Ala
500		505 510
Ile Lys Gly Ser	Asn Leu Ser Phe Ile	Cys Ser Ala Ala Ser Ser
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Ser Asp Ser Pro	Met Thr Phe Ala Trp	Lys Lys Asp Asn Glu Leu
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Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala Gln
545		550 555
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg Glu
560		565 570
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser Asn
575		580 585
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val Asn
590		595 600
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile Arg
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Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His Pro
620		625 630
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe Pro
635		640 645
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp Val
650		655 660
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr Ser
665		670 675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala Thr
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695		700 705
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile Ala
710		715 720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp Ser
725		730 735
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn Gln
740		745 750

F00T20-E060600

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
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 770 775 780
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
 785 790 795
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
 800 805 810
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 815 820 825
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
 830 835 840
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 845 850 855
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 860 865 870
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 875 880 885
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 890 895 900
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
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 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 920 925 930
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 935 940 945
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 950 955 960
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 965 970 975
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 980 985 990
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 995 1000 1005
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu

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Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
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Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

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<400> 296

cctaaactga actggacca 19

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100740-6062000

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F00T20-606060

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gaggaggcag aacagcctgc ctggttccat cagccctggc gccaggcgcc 400

00000000-00000000

Figure 1 consists of 12 line drawings of the head and thorax of the fly species, arranged in two rows of six. The drawings illustrate various morphological features, including the eye, antenna, and wing venation. The top row shows the head and thorax from a dorsal view, while the bottom row shows the head and thorax from a ventral view. The drawings are labeled with numbers 1 through 12, corresponding to the species listed in the caption.

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<212> DNA
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cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgaggggctgg 100
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[illegible]

Figure 1. The effect of the concentration of the *Agrobacterium* strain on the transformation efficiency of *Agrobacterium* strain 101. The concentration of the *Agrobacterium* strain 101 was varied from 10⁶ to 10⁹ cells/ml. The transformation efficiency was determined by the number of transformants per 10⁶ cells of the *Agrobacterium* strain 101. The data are the mean \pm SD of three independent experiments.

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				20					25					30	
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	
				35					40					45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	
				50					55					60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	
				65					70					75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	
				80					85					90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	
				95					100					105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	
				110					115					120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	
				125					130					135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	
				140					145					150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	
				155					160					165	

Thr Cys Val Asp	Val Asp Glu Cys Ala	Thr Gly Arg Ala Ser Cys
170		175 180
Pro Arg Phe Arg	Gln Cys Val Asn Thr	Phe Gly Ser Tyr Ile Cys
185		190 195
Lys Cys His Lys	Gly Phe Asp Leu Met	Tyr Ile Gly Gly Lys Tyr
200		205 210
Gln Cys His Asp	Ile Asp Glu Cys Ser	Leu Gly Gln Tyr Gln Cys
215		220 225
Ser Ser Phe Ala	Arg Cys Tyr Asn Val	Arg Gly Ser Tyr Lys Cys
230		235 240
Lys Cys Lys Glu	Gly Tyr Gln Gly Asp	Gly Leu Thr Cys Val Tyr
245		250 255
Ile Pro Lys Val	Met Ile Glu Pro Ser	Gly Pro Ile His Val Pro
260		265 270
Lys Gly Asn Gly	Thr Ile Leu Lys Gly	Asp Thr Gly Asn Asn Asn
275		280 285
Trp Ile Pro Asp	Val Gly Ser Thr Trp	Trp Pro Pro Lys Thr Pro
290		295 300
Tyr Ile Pro Pro	Ile Ile Thr Asn Arg	Pro Thr Ser Lys Pro Thr
305		310 315
Thr Arg Pro Thr	Pro Lys Pro Thr Pro	Ile Pro Thr Pro Pro Pro
320		325 330
Pro Pro Pro Leu	Pro Thr Glu Leu Arg	Thr Pro Leu Pro Pro Thr
335		340 345
Thr Pro Glu Arg	Pro Thr Thr Gly Leu	Thr Thr Ile Ala Pro Ala
350		355 360
Ala Ser Thr Pro	Pro Gly Gly Ile Thr	Val Asp Asn Arg Val Gln
365		370 375
Thr Asp Pro Gln	Lys Pro Arg Gly Asp	Val Phe Ser Val Leu Val
380		385 390
His Ser Cys Asn	Phe Asp His Gly Leu	Cys Gly Trp Ile Arg Glu
395		400 405
Lys Asp Asn Asp	Leu His Trp Glu Pro	Ile Arg Asp Pro Ala Gly
410		415 420
Gly Gln Tyr Leu	Thr Val Ser Ala Ala	Lys Ala Pro Gly Gly Lys

100120-200000

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly		
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser		
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
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<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 316

gatggttcct gctcaagtgc cctg 24

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggacccacg tacg 24

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319

<211> 2110

<212> DNA

F00120-20220500

<400> 319

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caacaggtgc	ttgctcgggg	ctgaaggtga	cagtgccatc	acacactgtc	150
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cactccagca	tcagacatcc	agatcatatg	gctatttgag	agaccccaca	250
caatgcccac	atacttactg	ggctctgtga	ataagtctgt	ggttcctgac	300
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tatcaaccca	ctgcagttcc	ctgatgaagg	caattacatc	gtgaaggtca	400
acattcaggg	aaatggaact	ctatctgcc	gtcagaagat	acaagtcacg	450
gttgatgatc	ctgtcacaaa	gccagtgggt	cagattcatc	ctccctctgg	500
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gcactcggct	agcttaccaa	tggctaaaaa	atgggagacc	tgtccacacc	600
agctccacct	actccttttc	tccccaaaac	aatacccttc	atattgctcc	650
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tactgttgac	cttgagagg	ccatcctatt	tgattgttct	gctgattctc	850
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aagatgaaac	tcatttcaca	gttatcatca	cttccgtagg	actggagaag	1050
cttgcacaga	aaggaaaatc	attgtcacct	ttagcaagta	taactggaat	1100
atcactattt	ttgattatat	ccatgtgtct	tctcttccta	tggaaaaaat	1150
atcaacccta	caaagttata	aaacagaaac	tagaaggcag	gccagaaaca	1200
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<210> 320
<211> 450
<212> PRT
<213> Homo Sapien
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Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His
          20              25              30

Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
          35              40              45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
          50              55              60

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Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser	
				65					70					75	
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro	
				80					85					90	
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu	
				95					100					105	
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu	
				110					115					120	
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr	
				125					130					135	
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr	
				140					145					150	
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg	
				155					160					165	
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser	
				170					175					180	
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala	
				185					190					195	
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg	
				200					205					210	
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	
				215					220					225	
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	
				230					235					240	
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	
				245					250					255	
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	
				260					265					270	
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	
				275					280					285	
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	
				290					295					300	
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	
				305					310					315	
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu	

100120-2052000

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
440	445	450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatacctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcttcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

F00T20-20620660

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150
tggatgatag aattttatgc cccgtggtgc cctgcttgct aaaatcttca 200
accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250
ttgcgaaagt agatgtcaca gaggcagccag gactgagtgg acggtttatc 300
ataactgctc ttctactat ttatcattgt aaagatggtg aatttaggcg 350
ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400
aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450
gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500
gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550
catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600
ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgcag 650
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aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatggt 750
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gaatgccata agacaacgtc ctctgggtcc atcattggcc acagataaat 850
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900
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<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val
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Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn
20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

	215		220		225									
Ser	Glu	Ser	Ala	Gln	Pro	Leu	Lys	Lys	Val	Glu	Glu	Glu	Gln	Glu
				230					235					240
Ala	Asp	Glu	Glu	Asp	Val	Ser	Glu	Glu	Glu	Ala	Glu	Ser	Lys	Glu
				245					250					255
Gly	Thr	Asn	Lys	Asp	Phe	Pro	Gln	Asn	Ala	Ile	Arg	Gln	Arg	Ser
				260					265					270
Leu	Gly	Pro	Ser	Leu	Ala	Thr	Asp	Lys	Ser					
				275					280					

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

F00740-20620660

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccctg gcagtcctgg tgctgttgc ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcgtaac taattcaaca 50

aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100

ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtagc 150

acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

tacctggctc accctgtgaa tgccatacaa ctggtgaagc ggctaaacac 450

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caatgctgag tgtggatgac tgctttggga tgggccgctc ggctacaat 700

gaaggggact attatcatc ggtgttgtgg atggagcagg tgctaaagca 750

F00120-EB2000

cctaccagaa aaaaaaaaaa 2168

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val
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20 25 30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys
35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val
80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu
95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg
110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala
125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile
140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser
155 160 165

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170					175					180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln
185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu
200 205 210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His	230	235	240
Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu	245	250	255
Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu	260	265	270
Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480

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<220>
<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 337

gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

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agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200
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Val Leu Thr Ser	Arg Ala Thr Leu Ser	Thr Leu Ala Val	Ala Val		
	110		115		120
Asn Arg Thr Val	Ala His His Phe Pro	Arg Leu Leu Tyr	Phe Thr		
	125		130		135
Gly Gln Arg Gly	Ala Arg Ala Pro Ala	Gly Met Gln Val	Val Ser		
	140		145		150
His Gly Asp Glu	Arg Pro Ala Trp Leu	Met Ser Glu Thr	Leu Arg		
	155		160		165
His Leu His Thr	His Phe Gly Ala Asp	Tyr Asp Trp Phe	Phe Ile		
	170		175		180
Met Gln Asp Asp	Thr Tyr Val Gln Ala	Pro Arg Leu Ala	Ala Leu		
	185		190		195
Ala Gly His Leu	Ser Ile Asn Gln Asp	Leu Tyr Leu Gly	Arg Ala		
	200		205		210
Glu Glu Phe Ile	Gly Ala Gly Glu Gln	Ala Arg Tyr Cys	His Gly		
	215		220		225
Gly Phe Gly Tyr	Leu Leu Ser Arg Ser	Leu Leu Leu Arg	Leu Arg		
	230		235		240
Pro His Leu Asp	Gly Cys Arg Gly Asp	Ile Leu Ser Ala	Arg Pro		
	245		250		255
Asp Glu Trp Leu	Gly Arg Cys Leu Ile	Asp Ser Leu Gly	Val Gly		
	260		265		270
Cys Val Ser Gln	His Gln Gly Gln Gln	Tyr Arg Ser Phe	Glu Leu		
	275		280		285
Ala Lys Asn Arg	Asp Pro Glu Lys Glu	Gly Ser Ser Ala	Phe Leu		
	290		295		300
Ser Ala Phe Ala	Val His Pro Val Ser	Glu Gly Thr Leu	Met Tyr		
	305		310		315
Arg Leu His Lys	Arg Phe Ser Ala Leu	Glu Leu Glu Arg	Ala Tyr		
	320		325		330
Ser Glu Ile Glu	Gln Leu Gln Ala Gln	Ile Arg Asn Leu	Thr Val		
	335		340		345
Leu Thr Pro Glu	Gly Glu Ala Gly Leu	Ser Trp Pro Val	Gly Leu		
	350		355		360

100120-2000000

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	620	625	630

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<212> DNA
<213> Homo Sapien
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tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100
ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
accaaacact gtgacaaagc agagtctctc agttctgaaa atgttaaagt 400
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<210> 341
<211> 318
<212> PRT
<213> Homo Sapien
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Met	Leu	Ser	Glu	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly	
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Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
				20					25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
				35					40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
				50					55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
				65					70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
				80					85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
				95					100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
				110					115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
				125					130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
				140					145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
				155					160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
				170					175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
				185					190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
				200					205					210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
				215					220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
				230					235					240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
				245					250					255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

	260		265		270
Cys Ser Asp Met	Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln				
	275		280		285
Met His Val Met	Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly				
	290		295		300
His Ile Phe Asn Asp	Ala Leu Val Phe Leu Pro Pro Asn Gly Ser				
	305		310		315

Asp Asn Asp

<210> 342

<211> 23

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaagtc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

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<400> 345

<210> 346

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<400> 346

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaataacgactcactataggggtcagaaaagcgcaacagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

<212> DNA

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<400> 355

ctatgaaatt aaccctcact aaaggagct gccgatccca ctggtatt 48

<210> 356

<211> 46

<212> DNA

<213> Artificial Sequence

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<400> 356

ggattctaatt acgactcact atagggcgga tcctggccgg cctctg 46

<210> 357

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<400> 357

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<210> 358

<211> 47

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<400> 358

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<210> 359

<211> 48

<212> DNA

<213> Artificial Sequence

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<400> 359

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<211> 48
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<400> 360
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<210> 361
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<400> 361
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<400> 362
ggattctaatacgcactcactatagggcccgctcgctcctgctcctg 47

<210> 363
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<212> DNA
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<400> 363
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<400> 364

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ggattctaatacgcactcactatagggccccctctgccttcctgtcc47

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Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro
				20					25					30
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
				35					40					45
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
				50					55					60
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser
				65					70					75
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
				80					85					90
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
				95					100					105
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
				110					115					120
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
				125					130					135
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
				140					145					150
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
				155					160					165
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
				170					175					180

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<210> 383
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<210> 384
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<400> 384
cagctgccct tccccaacca 20

<210> 385
<211> 18
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<400> 385
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<212> DNA

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<400> 387

gggccatcac agctccct 18

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<210> 405
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gggacgtgct tctacaagaa cag 23

<210> 406
<211> 26
<212> DNA
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<220>
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<210> 407
<211> 31
<212> DNA
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tattcagagt ttccattgg cagtgccagt t 31

<210> 408
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cgatcttctc cacccaggag cgg 23

<210> 410
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<211> 23

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ctccctgaat ggcagcctga gca 23

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<211> 21

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<223> Synthetic oligonucleotide probe

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<211> 22

<213> Artificial Sequence

<220>

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ccctgtttcc ctatgcatca ct 22

<211> 21

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<223> Synthetic oligonucleotide probe

tcaaccctg accctttcct a 21

<211> 24

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gggactgaac tgccagcttc 20

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<210> 421

<211> 21

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<212> DNA

<213> Homo Sapien

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 cttcttctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150
 tcaaattccag caatcgaacc ccagtggtac aggaatttga aagtgtggaa 200
 ctgtcttgca tcattacgga ttgcagaca agtgacccca ggatcgagtg 250
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
 ttcagggaga cttggcgggt cgtgcagaaa tactgggggaa gacatccctg 350
 aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400
 cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450
 ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500
 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550
 ccggcctcac tacagctggg atcgcaatga tgtaccactg cccacggatt 600
 ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650
 acaggcactt tgggtgttcac tgctgttcac aaggacgact ctgggcagta 700
 ctactgcatt gcttccaatg acgcaggctc agccagggtg gaggagcagg 750

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[illegible]

[illegible]

一、政治思想
 二、工作表现
 三、生活作风
 四、其他情况
 五、结论
 六、备注

$\langle 211 \rangle$ 310

<213> Homo Sapien

Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu
1 5 10 15

Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu
35 40 45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
50 55 60

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
65 70 75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
80 85 90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
95 100 105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
110 115 120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
125 130 135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
140 145 150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
155 160 165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
170 175 180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
185 190 195

姓名	性别	年龄	职业	住址	联系电话	备注
王德胜	男	45	教师	XX市XX区XX路XX号	138XXXXXXX	
李小明	男	32	工程师	XX市XX区XX路XX号	139XXXXXXX	
张小红	女	28	护士	XX市XX区XX路XX号	137XXXXXXX	
赵国强	男	55	退休	XX市XX区XX路XX号	136XXXXXXX	
陈丽娟	女	40	会计	XX市XX区XX路XX号	135XXXXXXX	
周大伟	男	38	医生	XX市XX区XX路XX号	134XXXXXXX	
吴小芳	女	25	学生	XX市XX区XX路XX号	133XXXXXXX	
郑伟明	男	50	经理	XX市XX区XX路XX号	132XXXXXXX	
孙小红	女	35	律师	XX市XX区XX路XX号	131XXXXXXX	
马国强	男	42	农民	XX市XX区XX路XX号	130XXXXXXX	
朱小华	女	30	公务员	XX市XX区XX路XX号	129XXXXXXX	
徐伟明	男	48	教授	XX市XX区XX路XX号	128XXXXXXX	
黄小红	女	22	学生	XX市XX区XX路XX号	127XXXXXXX	
周大伟	男	52	工程师	XX市XX区XX路XX号	126XXXXXXX	
吴小芳	女	33	护士	XX市XX区XX路XX号	125XXXXXXX	
郑伟明	男	40	经理	XX市XX区XX路XX号	124XXXXXXX	
孙小红	女	27	学生	XX市XX区XX路XX号	123XXXXXXX	
马国强	男	58	退休	XX市XX区XX路XX号	122XXXXXXX	
朱小华	女	37	会计	XX市XX区XX路XX号	121XXXXXXX	
徐伟明	男	43	医生	XX市XX区XX路XX号	120XXXXXXX	
黄小红	女	24	学生	XX市XX区XX路XX号	119XXXXXXX	
周大伟	男	53	工程师	XX市XX区XX路XX号	118XXXXXXX	
吴小芳	女	34	护士	XX市XX区XX路XX号	117XXXXXXX	
郑伟明	男	41	经理	XX市XX区XX路XX号	116XXXXXXX	
孙小红	女	26	学生	XX市XX区XX路XX号	115XXXXXXX	
马国强	男	59	退休	XX市XX区XX路XX号	114XXXXXXX	
朱小华	女	36	会计	XX市XX区XX路XX号	113XXXXXXX	
徐伟明	男	44	医生	XX市XX区XX路XX号	112XXXXXXX	
黄小红	女	23	学生	XX市XX区XX路XX号	111XXXXXXX	
周大伟	男	54	工程师	XX市XX区XX路XX号	110XXXXXXX	
吴小芳	女	35	护士	XX市XX区XX路XX号	109XXXXXXX	
郑伟明	男	42	经理	XX市XX区XX路XX号	108XXXXXXX	
孙小红	女	25	学生	XX市XX区XX路XX号	107XXXXXXX	
马国强	男	60	退休	XX市XX区XX路XX号	106XXXXXXX	
朱小华	女	38	会计	XX市XX区XX路XX号	105XXXXXXX	
徐伟明	男	45	医生	XX市XX区XX路XX号	104XXXXXXX	
黄小红	女	21	学生	XX市XX区XX路XX号	103XXXXXXX	
周大伟	男	55	工程师	XX市XX区XX路XX号	102XXXXXXX	
吴小芳	女	36	护士	XX市XX区XX路XX号	101XXXXXXX	
郑伟明	男	43	经理	XX市XX区XX路XX号	100XXXXXXX	
孙小红	女	24	学生	XX市XX区XX路XX号	099XXXXXXX	
马国强	男	61	退休	XX市XX区XX路XX号	098XXXXXXX	
朱小华	女	39	会计	XX市XX区XX路XX号	097XXXXXXX	
徐伟明	男	46	医生	XX市XX区XX路XX号	096XXXXXXX	
黄小红	女	20	学生	XX市XX区XX路XX号	095XXXXXXX	
周大伟	男	56	工程师	XX市XX区XX路XX号	094XXXXXXX	
吴小芳	女	37	护士	XX市XX区XX路XX号	093XXXXXXX	
郑伟明	男	44	经理	XX市XX区XX路XX号	092XXXXXXX	
孙小红	女	23	学生	XX市XX区XX路XX号	091XXXXXXX	
马国强	男	62	退休	XX市XX区XX路XX号	090XXXXXXX	
朱小华	女	40	会计	XX市XX区XX路XX号	089XXXXXXX	
徐伟明	男	47	医生	XX市XX区XX路XX号	088XXXXXXX	
黄小红	女	19	学生	XX市XX区XX路XX号	087XXXXXXX	
周大伟	男	57	工程师	XX市XX区XX路XX号	086XXXXXXX	
吴小芳	女	38	护士	XX市XX区XX路XX号	085XXXXXXX	
郑伟明	男	45	经理	XX市XX区XX路XX号	084XXXXXXX	
孙小红	女	22	学生	XX市XX区XX路XX号	083XXXXXXX	
马国强	男	63	退休	XX市XX区XX路XX号	082XXXXXXX	
朱小华	女	41	会计	XX市XX区XX路XX号	081XXXXXXX	
徐伟明	男	48	医生			